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Welcome to the SIB BLAST Network Service

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In case of problems, please read the [online BLAST help](#).
If your question is not covered, please contact [<helpdesk@expasy.org>](mailto:helpdesk@expasy.org).

NCBI BLAST program reference [PMID:9254694]:

Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W., Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. 25:3389-3402(1997).

=====

Query length: 270 AA (of which 6% low-complexity regions filtered out)

Date run: 2004-04-30 21:23:21 UTC+0100 on sib-gm1.unil.ch

Program: NCBI BLASTP 1.5.4-Paracel [2003-06-05]

Database: EXPASY/UniProt

1,459,789 sequences; 465,400,423 total letters

[Taxonomic view](#)

[NiceBlast view](#)

[Printable view](#)

List of potentially matching sequences

Send selected sequences to

☐ Include query sequence

Db AC	Description	Score E-value
<input type="checkbox"/> tr Q9ZLD5	Outer membrane protein/porin [HOPE] [Helicobacter pylo...	539 e-152
<input type="checkbox"/> tr O25410	Outer membrane protein (OMP15) [HP0706] [Helicobacter ...	527 e-149
<input type="checkbox"/> tr Q9X750	HopW protein precursor [HOPW] [Helicobacter pylori (Ca...	136 4e-31
<input type="checkbox"/> tr Q9ZJB9	Putative outer membrane protein [JHP1394] [Helicobacte...	135 5e-31
<input type="checkbox"/> tr O26031	Hypothetical protein HP1501 [HP1501] [Helicobacter pyl...	135 7e-31
<input type="checkbox"/> tr O25382	Outer membrane protein (OMP14) [HP0671] [Helicobacter ...	115 9e-25
<input type="checkbox"/> tr Q9ZLG6	Putative outer membrane protein [JHP0614] [Helicobacte...	113 3e-24
<input type="checkbox"/> tr Q9ZMI3	Putative outer membrane protein [JHP0237] [Helicobacte...	98 1e-19
<input type="checkbox"/> tr Q9X752	HopZ protein precursor [HOPZ] [Helicobacter pylori (Ca...	98 1e-19
<input type="checkbox"/> tr O25034	Outer membrane protein (OMP7) [HP0252] [Helicobacter p...	98 2e-19

Alignments

tr Q9ZLD5 Outer membrane protein/porin [HOPE] [Helicobacter pylori J99] 270 AA
(Campylobacter pylori J99)]

align

Score = 539 bits (1389), Expect = e-152
Identities = 254/270 (94%), Positives = 254/270 (94%)

Query: 1 MKKFXXXXXXXXXXXXXXXXXXEGDGVYIGTNYQLGQARLNSNIYNTGDCTGSVVGCPPGLT 60
MKKF EGDGVYIGTNYQLGQARLNSNIYNTGDCTGSVVGCPPGLT
Sbjct: 1 MKKFVALGLLSAVLSSSLLAEGDGVYIGTNYQLGQARLNSNIYNTGDCTGSVVGCPPGLT 60

Query: 61 ANKHNPGGTNINWHSKYANGALNGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHA 120
ANKHNPGGTNINWHSKYANGALNGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHA
Sbjct: 61 ANKHNPGGTNINWHSKYANGALNGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHA 120

Query: 121 DLGKQVYAPNKIQLDMVSWGVGSDLLADIIDKDNASFGIFGGVAIGGNTWKSSAANYWKE 180
DLGKQVYAPNKIQLDMVSWGVGSDLLADIIDKDNASFGIFGGVAIGGNTWKSSAANYWKE
Sbjct: 121 DLGKQVYAPNKIQLDMVSWGVGSDLLADIIDKDNASFGIFGGVAIGGNTWKSSAANYWKE 180

Query: 181 QIIIEAKGPDVCTPTYCNPAPYSTNTSTVAFQVWLNFGVRANIYKHNGVEFGVRVPLLIN 240
QIIIEAKGPDVCTPTYCNPAPYSTNTSTVAFQVWLNFGVRANIYKHNGVEFGVRVPLLIN
Sbjct: 181 QIIIEAKGPDVCTPTYCNPAPYSTNTSTVAFQVWLNFGVRANIYKHNGVEFGVRVPLLIN 240

Query: 241 KFLSAGPNATNLYYHLKRDYSLYLGNYTF 270
KFLSAGPNATNLYYHLKRDYSLYLGNYTF
Sbjct: 241 KFLSAGPNATNLYYHLKRDYSLYLGNYTF 270

tr O25410 Outer membrane protein (OMP15) [HP0706] [Helicobacter pylori] 273 AA
(Campylobacter pylori)]

align

Score = 527 bits (1358), Expect = e-149
Identities = 248/270 (91%), Positives = 249/270 (91%)

Query: 1 MKKFXXXXXXXXXXXXXXXXXXEGDGVYIGTNYQLGQARLNSNIYNTGDCTGSVVGCPPGLT 60
MKKF EGDGVYIGTNYQLGQARLNSNIYNTGDCTGSVVGCPPGLT
Sbjct: 4 MKKFVALGLLSAVLSSSLLAEGDGVYIGTNYQLGQARLNSNIYNTGDCTGSVVGCPPGLT 63

Query: 61 ANKHNPGGTNINWHSKYANGALNGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHA 120
ANKHNPGGTNINWH+KYANGALNG GLNVGYKKFFQFKS DMTSKWFGFRVYGLFDYGHA
Sbjct: 64 ANKHNPGGTNINWHAKYANGALNGLGLNVGYKKFFQFKSFDMTSKWFGFRVYGLFDYGHA 123

Query: 121 DLGKQVYAPNKIQLDMVSWGVGSDLLADIIDKDNASFGIFGGVAIGGNTWKSSAANYWKE 180
LGKQVYAPNKIQLDMVSWGVGSDLLADIID DNASFGIFGGVAIGGNTWKSSAANYWKE
Sbjct: 124 TLGKQVYAPNKIQLDMVSWGVGSDLLADIIDNDNASFGIFGGVAIGGNTWKSSAANYWKE 183

Query: 181 QIIIEAKGPDVCTPTYCNPAPYSTNTSTVAFQVWLNFGVRANIYKHNGVEFGVRVPLLIN 240
QIIIEAKGPDVCTPTYCNPAPYST TSTVAFQVWLNFGVRANIYKHNGVEFGVRVPLLIN
Sbjct: 184 QIIIEAKGPDVCTPTYCNPAPYSTKTSTVAFQVWLNFGVRANIYKHNGVEFGVRVPLLIN 243

Query: 241 KFLSAGPNATNLYYHLKRDYSLYLGNYTF 270
KFLSAGPNATNLYYHLKRDYSLYLGNYTF

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NCBI BLAST program reference [PMID:9254694]:

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=====

Query length: 27 AA

Date run: 2004-04-30 22:22:55 UTC+0100 on sib-gml.unil.ch

Program: NCBI BLASTP 1.5.4-Paracel [2003-06-05]

Database: EXPASY/UniProt

1,459,789 sequences; 465,400,423 total letters

List of potentially matching sequences

Send selected sequences to ☐ Include query sequence

Db AC

Description

Score E-value

- | | | | | |
|--------------------------|---------------------------|---|--------------------|-------|
| <input type="checkbox"/> | tr Q9R4J2 | 31 kDa major NONSELECTIVE porin protein (Fragment) [He... | 79 | 8e-15 |
| <input type="checkbox"/> | tr Q9ZLD5 | Outer membrane protein/porin [HOPE] [Helicobacter pylo... | 77 | 3e-14 |
| <input type="checkbox"/> | tr Q25410 | Outer membrane protein (OMP15) [HP0706] [Helicobacter ... | 77 | 3e-14 |
| <input type="checkbox"/> | tr Q7RFV7 | Hypothetical protein [PY04595] [Plasmodium yoelii yoelii] | 29 | 9.5 |

Graphical overview of the alignments

to resubmit your query after masking regions matching [PROSITE](#) profiles or Pfam HMMs

([?](#) Help) (use [ScanProsite](#) for more details about PROSITE matches)

Profile hits				
Pfam hits				
	Matches on query sequence			Mat
Submission	1			1
Q9R4J2				
Q9ZLD5				
O25410				
Q7RFV7				
Submission	1			
Identity	0	25	50	75 100%

Alignments

tr Q9R4J2 31 kDa major NONSELECTIVE porin protein (Fragment) 30 AA
 [Helicobacter pylori (Campylobacter pylori)] [align](#)

Score = 78.7 bits (178), Expect = 8e-15
 Identities = 27/30 (90%), Positives = 27/30 (90%), Gaps = 3/30 (10%)

Query: 1 EGDGVYIGTNYQ---ARLNSNIYNTGDXTG 27
 EGDGVYIGTNYQ ARLNSNIYNTGD TG
 Sbjct: 1 EGDGVYIGTNYQLGQARLNSNIYNTGDXTG 30

tr Q9ZLD5 Outer membrane protein/porin [HOPE] [Helicobacter pylori J99] 270 AA
 (Campylobacter pylori J99)] [align](#)

Score = 77.0 bits (174), Expect = 3e-14
 Identities = 26/30 (86%), Positives = 26/30 (86%), Gaps = 3/30 (10%)

Query: 1 EGDGVYIGTNYQ---ARLNSNIYNTGDXTG 27
 EGDGVYIGTNYQ ARLNSNIYNTGD TG
 Sbjct: 21 EGDGVYIGTNYQLGQARLNSNIYNTGDCTG 50

tr O25410 Outer membrane protein (OMP15) [HP0706] [Helicobacter pylori] 273 AA
 (Campylobacter pylori)] [align](#)

Score = 77.0 bits (174), Expect = 3e-14
 Identities = 26/30 (86%), Positives = 26/30 (86%), Gaps = 3/30 (10%)

Query: 1 EGDGVYIGTNYQ---ARLNSNIYNTGDXTG 27
 EGDGVYIGTNYQ ARLNSNIYNTGD TG
 Sbjct: 24 EGDGVYIGTNYQLGQARLNSNIYNTGDCTG 53

tr Q7RFV7 **Hypothetical protein [PY04595] [Plasmodium yoelii yoelii]** 1048 AA

align

Score = 28.6 bits (60), Expect = 9.5

Identities = 12/22 (54%), Positives = 12/22 (54%), Gaps = 9/22 (40%)

Query: 6 YIGTNYQARLNS-----NIYNT 22

Y GTN LNS NIYNT

Sbjct: 490 YKGTN----LNSDPYNNIYNT 507

Database: EXPASY/UniProt

Posted date: Apr 25, 2004 4:51 AM

Number of letters in database: 465,400,423

Number of sequences in database: 1,459,789

Lambda	K	H
0.340	0.282	1.71

Gapped

Lambda	K	H
0.294	0.110	0.610

Matrix: PAM30

Gap Penalties: Existence: 9, Extension: 1
length of query: 27

length of database: 465,400,423

effective HSP length: 18

effective length of query: 9

effective length of database: 439,124,221

effective search space: 3952117989

effective search space used: 3952117989

T: 16

A: 40

X1: 15 (7.4 bits)

X2: 35 (14.8 bits)

X3: 58 (24.6 bits)

S1: 41 (21.9 bits)

S2: 60 (28.6 bits)

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Molecular detection of methionine in rat brain using specific antibodies

Amara A ; Coussemacq M; Geffard M.

Laboratoire d'Immunologie et Pathologie, Universite de Bordeaux II, France.

Neuroscience letters (IRELAND) Feb 13 1995 , 185 (3) p147-50,
ISSN 0304-3940 Journal Code: N7N

Languages: ENGLISH

Document type: Journal Article

Record type: Completed

Subfile: INDEX MEDICUS

In order to study the localization of methionine in rat brain, an immunological approach was developed by raising **antibodies** directed against this amino acid. Methionine was conjugated to bovine serum albumin (BSA) or human serum albumin (HSA) via glutaraldehyde. The conjugates were then reduced by sodium borohydride and injected alternately into rabbits.

Antibody affinity and specificity were evaluated using an adapted ELISA method, by competition experiments between conjugated methionine and related conjugated compounds, pre-incubated with anti-methionine **antibodies** diluted at 1/20,000. The resulting cross-reactivity ratios, calculated at half-displacement, showed that glutaraldehyde-methionine conjugate (methionine-G-BSA) was the best recognized compound. Non-reduced methionine conjugate (methionine=G=BSA) and the related-conjugated molecules such as homocysteine, homocysteic acid, cysteine, cystathionine and glutamate were not recognized at all. **Antibodies** to methionine were directed against a glutaraldehyde-methionine epitope and their very high affinity and specificity made them reliable tools for molecular detection of methionine in rat brain. Using purified **antibodies** diluted at 1/20,000, motoneurons were found to be the most methionine-immunoreactive cell bodies in glutaraldehyde-fixed rat brain sections.

Tags: Animal; Support, Non-U.S. Gov't

Descriptors: **Antibodies** --immunology--IM; *Methionine--pharmacology--PD ; Brain; Enzyme-Linked Immunosorbent Assay; Glutaral; Immunohistochemistry; Methionine--immunology--IM; Motor Neurons; Rabbits; Rats

CAS Registry No.: 0 (Antibodies); 111-30-8 (Glutaral); 7005-18-7 (Methionine)

Record Date Created: 19950621

?logoff hold

STIC-ILL

From: Portner, Ginny
Sent: Thursday, January 25, 2001 11:38 AM
To: STIC-ILL
Subject: porin/hp

Mile
QRI. A47 A3

Infect. Immun., April 1994, pages 1392-1399, Vol 62, No. 4
Copyright © 1994, American Society for Microbiology
Immunobiological activities of Helicobacter pylori porins

MA Tufano, F Rossano, P Catalanotti, G Liguori, C Capasso, MT Ceccarelli and P Marinelli
Istituto di Microbiologia, Seconda Universita di Napoli, Italy.

Ginny Portner
Art Unit 1645
CM1-7e13
(703) 308-7543

STIC-ILL

APL

From: Portner, Ginny
Sent: Wednesday, June 13, 2001 8:26 AM
To: STIC-ILL
Subject: 09/559,814

Isolation and characterization of a family of porin proteins from *Helicobacter pylori*.

Exner MM; Doig P; Trust TJ; Hancock RE

Department of Microbiology and Immunology, University of British Columbia, Vancouver, Canada.

Infection and immunity (UNITED STATES) Apr 1995, 63 (4) p1567-72,

ISSN 0019-9567 Journal Code: GO7

Contract/Grant No.: R01AI29927-01A2, AI, NIAID

Languages: ENGLISH

Document type: Journal Article

Record type: Completed

Immunobiological activities of *Helicobacter pylori* porins.

Tufano MA; Rossano F; Catalanotti P; Liguori G; Capasso C; Ceccarelli MT; Marinelli P

Istituto di Microbiologia, Seconda Universita di Napoli, Italy.

Infection and immunity (UNITED STATES) Apr 1994, 62 (4) p1392-9,

ISSN 0019-9567 Journal Code: GO7

Languages: ENGLISH

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Ginny Portner

CM-1, 7e13

Art Unit 1645

(703) 308-7543

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Query length: 270 AA (of which 6% low-complexity regions filtered out)

Date run: 2004-04-30 21:23:21 UTC+0100 on sib-gml.unil.ch

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[Taxonomic view](#)[NiceBlast view](#)[Printable view](#)

List of potentially matching sequences

Send selected sequences to ☒ Include query sequence

Note #

↓

Db	AC	Description	Score	E-value
<input checked="" type="checkbox"/>	tr Q9ZLD5	Outer membrane protein/porin [HOPE] [Helicobacter pylo...	539	e-152
<input checked="" type="checkbox"/>	tr Q25410	Outer membrane protein (OMP15) [HP0706] [Helicobacter ...	527	e-149
<input checked="" type="checkbox"/>	tr Q9X750	HopW protein precursor [HOPW] [Helicobacter pylori (Ca...	136	4e-31
<input checked="" type="checkbox"/>	tr Q9ZJB9	Putative outer membrane protein [JHP1394] [Helicobacte...	135	5e-31
<input type="checkbox"/>	tr Q26031	Hypothetical protein HP1501 [HP1501] [Helicobacter pyl...	135	7e-31
<input type="checkbox"/>	tr Q25382	Outer membrane protein (OMP14) [HP0671] [Helicobacter ...	115	9e-25
<input type="checkbox"/>	tr Q9ZLG6	Putative outer membrane protein [JHP0614] [Helicobacte...	113	3e-24
<input type="checkbox"/>	tr Q9ZMI3	Putative outer membrane protein [JHP0237] [Helicobacte...	98	1e-19
<input type="checkbox"/>	tr Q9X752	HopZ protein precursor [HOPZ] [Helicobacter pylori (Ca...	98	1e-19
<input type="checkbox"/>	tr Q25034	Outer membrane protein (OMP7) [HP0252] [Helicobacter p...	98	2e-19

Alignments

tr Q9ZLD5 Outer membrane protein/porin [HOPE] [Helicobacter pylori J99] 270 AA
(Campylobacter pylori J99)]

align

Score = 539 bits (1389), Expect = e-152
Identities = 254/270 (94%), Positives = 254/270 (94%)

Query: 1 MKKFXXXXXXXXXXXXXXXXXXEGDGVYIGTNYQLGQARLNSNIYNTGDC TGSVVGCPPGLT 60
MKKF EGDGVYIGTNYQLGQARLNSNIYNTGDC TGSVVGCPPGLT
Sbjct: 1 MKKFVALGLLSAVLSSSLLAEGDGVYIGTNYQLGQARLNSNIYNTGDC TGSVVGCPPGLT 60

Query: 61 ANKHNPGGTNINWHSKYANGALNGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHA 120
ANKHNPGGTNINWHSKYANGALNGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHA
Sbjct: 61 ANKHNPGGTNINWHSKYANGALNGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHA 120

Query: 121 DLGKQVYAPNKIQLDMSWGVGSDLLADIIDKDNASFGIFGGVAIGGNTWKSSAANYWKE 180
DLGKQVYAPNKIQLDMSWGVGSDLLADIIDKDNASFGIFGGVAIGGNTWKSSAANYWKE
Sbjct: 121 DLGKQVYAPNKIQLDMSWGVGSDLLADIIDKDNASFGIFGGVAIGGNTWKSSAANYWKE 180

Query: 181 QIIIEAKGPDVCTPTYCNPAPYSTNTSTVAFQVWLNFGVRANIYKHNGVEFGVRVPLLIN 240
QIIIEAKGPDVCTPTYCNPAPYSTNTSTVAFQVWLNFGVRANIYKHNGVEFGVRVPLLIN
Sbjct: 181 QIIIEAKGPDVCTPTYCNPAPYSTNTSTVAFQVWLNFGVRANIYKHNGVEFGVRVPLLIN 240

Query: 241 KFLSAGPNATNLYYHLKRDYSLYLGYN YTF 270
KFLSAGPNATNLYYHLKRDYSLYLGYN YTF
Sbjct: 241 KFLSAGPNATNLYYHLKRDYSLYLGYN YTF 270

tr O25410 Outer membrane protein (OMP15) [HP0706] [Helicobacter pylori] 273 AA
(Campylobacter pylori)]

align

Score = 527 bits (1358), Expect = e-149
Identities = 248/270 (91%), Positives = 249/270 (91%)

Query: 1 MKKFXXXXXXXXXXXXXXXXXXEGDGVYIGTNYQLGQARLNSNIYNTGDC TGSVVGCPPGLT 60
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Query: 61 ANKHNPGGTNINWHSKYANGALNGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHA 120
ANKHNPGGTNINWH+KYANGALNG GLNVGYKKFFQFKS DMTSKWFGFRVYGLFDYGHA
Sbjct: 64 ANKHNPGGTNINWHAKYANGALNGLGLNVGYKKFFQFKSFDMTSKWFGFRVYGLFDYGHA 123

Query: 121 DLGKQVYAPNKIQLDMSWGVGSDLLADIIDKDNASFGIFGGVAIGGNTWKSSAANYWKE 180
LGKQVYAPNKIQLDMSWGVGSDLLADIID DNASFGIFGGVAIGGNTWKSSAANYWKE
Sbjct: 124 TLGKQVYAPNKIQLDMSWGVGSDLLADIIDNDNASFGIFGGVAIGGNTWKSSAANYWKE 183

Query: 181 QIIIEAKGPDVCTPTYCNPAPYSTNTSTVAFQVWLNFGVRANIYKHNGVEFGVRVPLLIN 240
QIIIEAKGPDVCTPTYCNPAPYST TSTVAFQVWLNFGVRANIYKHNGVEFGVRVPLLIN
Sbjct: 184 QIIIEAKGPDVCTPTYCNPAPYSTTKTSTVAFQVWLNFGVRANIYKHNGVEFGVRVPLLIN 243

Query: 241 KFLSAGPNATNLYYHLKRDYSLYLGYN YTF 270
KFLSAGPNATNLYYHLKRDYSLYLGYN YTF

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Db	AC	Description	Score	E-value
<input type="checkbox"/>	tr Q9R4J2	31 kDa major NONSELECTIVE porin protein (Fragment) [He...	79	8e-15
<input type="checkbox"/>	tr Q9ZLD5	Outer membrane protein/porin [HOPE] [Helicobacter pylo...	77	3e-14
<input type="checkbox"/>	tr Q25410	Outer membrane protein (OMP15) [HP0706] [Helicobacter ...	77	3e-14
<input type="checkbox"/>	tr Q7RFV7	Hypothetical protein [PY04595] [Plasmodium yoelii yoelii]	29	9.5

Graphical overview of the alignments

[Click here](#)

to resubmit your query after masking regions matching [PROSITE](#) profiles or [Pfam](#) HMMs

([?](#) Help) (use [ScanProsite](#) for more details about PROSITE matches)

Profile hits			
Pfam hits			
	Matches on query sequence		Mat
Submission	1		1
Q9R4J2			
Q9ZLD5			
Q25410			
Q7RFV7			
Submission	1		
Identity	0	25	50 75 100%

Alignments

tr Q9R4J2 31 kDa major NONSELECTIVE porin protein (Fragment) 30 AA
 [Helicobacter pylori (Campylobacter pylori)] [align](#)

Score = 78.7 bits (178), Expect = 8e-15
 Identities = 27/30 (90%), Positives = 27/30 (90%), Gaps = 3/30 (10%)

Query: 1 EGDGVYIGTNYQ---ARLNSNIYNTGDXTG 27
 EGDGVYIGTNYQ ARLNSNIYNTGD TG
 Sbjct: 1 EGDGVYIGTNYQLGQARLNSNIYNTGDXTG 30

tr Q9ZLD5 Outer membrane protein/porin [HOPE] [Helicobacter pylori J99] 270 AA
 (Campylobacter pylori J99)] [align](#)

Score = 77.0 bits (174), Expect = 3e-14
 Identities = 26/30 (86%), Positives = 26/30 (86%), Gaps = 3/30 (10%)

Query: 1 EGDGVYIGTNYQ---ARLNSNIYNTGDXTG 27
 EGDGVYIGTNYQ ARLNSNIYNTGD TG
 Sbjct: 21 EGDGVYIGTNYQLGQARLNSNIYNTGDCTG 50

tr Q25410 Outer membrane protein (OMP15) [HP0706] [Helicobacter pylori] 273 AA
 (Campylobacter pylori)] [align](#)

Score = 77.0 bits (174), Expect = 3e-14
 Identities = 26/30 (86%), Positives = 26/30 (86%), Gaps = 3/30 (10%)

Query: 1 EGDGVYIGTNYQ---ARLNSNIYNTGDXTG 27
 EGDGVYIGTNYQ ARLNSNIYNTGD TG
 Sbjct: 24 EGDGVYIGTNYQLGQARLNSNIYNTGDCTG 53

tr Q7RFV7 Hypothetical protein [PY04595] [Plasmodium yoelii yoelii] 1048 AA

align

Score = 28.6 bits (60), Expect = 9.5

Identities = 12/22 (54%), Positives = 12/22 (54%), Gaps = 9/22 (40%)

Query: 6 YIGTNYQARLNS-----NIYNT 22

Y GTN LNS NIYNT

Sbjct: 490 YKGTN----LNSDPYNNIYNT 507

Database: EXPASY/UniProt

Posted date: Apr 25, 2004 4:51 AM

Number of letters in database: 465,400,423

Number of sequences in database: 1,459,789

Lambda	K	H
0.340	0.282	1.71

Gapped

Lambda	K	H
0.294	0.110	0.610

Matrix: PAM30

Gap Penalties: Existence: 9, Extension: 1

length of query: 27

length of database: 465,400,423

effective HSP length: 18

effective length of query: 9

effective length of database: 439,124,221

effective search space: 3952117989

effective search space used: 3952117989

T: 16

A: 40

X1: 15 (7.4 bits)

X2: 35 (14.8 bits)

X3: 58 (24.6 bits)

S1: 41 (21.9 bits)

S2: 60 (28.6 bits)

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--	--------------------------	-------------------------------	----------------------------	----------------------------------	----------------------------

Molecular detection of methionine in rat brain using specific antibodies

Amara A ; Coussemacq M; Geffard M.

Laboratoire d'Immunologie et Pathologie, Universite de Bordeaux II, France.

Neuroscience letters (IRELAND) Feb 13 1995 , 185 (3) p147-50,
ISSN 0304-3940 Journal Code: N7N

Languages: ENGLISH

Document type: Journal Article

Record type: Completed

Subfile: INDEX MEDICUS

In order to study the localization of methionine in rat brain, an immunological approach was developed by raising **antibodies** directed against this amino acid. Methionine was conjugated to bovine serum albumin (BSA) or human serum albumin (HSA) via glutaraldehyde. The conjugates were then reduced by sodium borohydride and injected alternately into rabbits.

Antibody affinity and specificity were evaluated using an adapted ELISA method, by competition experiments between conjugated methionine and related conjugated compounds, pre-incubated with anti-methionine **antibodies** diluted at 1/20,000. The resulting cross-reactivity ratios, calculated at half-displacement, showed that glutaraldehyde-methionine conjugate (methionine-G-BSA) was the best recognized compound. Non-reduced methionine conjugate (methionine=G=BSA) and the related-conjugated molecules such as homocysteine, homocysteic acid, cysteine, cystathionine and glutamate were not recognized at all. **Antibodies** to methionine were directed against a glutaraldehyde-methionine epitope and their very high affinity and specificity made them reliable tools for molecular detection of methionine in rat brain. Using purified **antibodies** diluted at 1/20,000, motoneurons were found to be the most methionine-immunoreactive cell bodies in glutaraldehyde-fixed rat brain sections.

Tags: Animal; Support, Non-U.S. Gov't

Descriptors: **Antibodies** --immunology--IM; *Methionine--pharmacology--PD ; Brain; Enzyme-Linked Immunosorbent Assay; Glutaral; Immunohistochemistry; Methionine--immunology--IM; Motor Neurons; Rabbits; Rats

CAS Registry No.: 0 (Antibodies); 111-30-8 (Glutaral); 7005-18-7 (Methionine)

Record Date Created: 19950621

?logoff hold

[ExPASy Home page](#) [Site Map](#) [Search ExPASy](#) [Contact us](#) [Proteomics tools](#) [Swiss-Prot](#)

Search for

Welcome to the SIB BLAST Network Service

If results of this search are reported or published, please mention that the computation was performed at the SIB using the BLAST network service. The SIB BLAST network service uses a server developed at SIB and the NCBI BLAST 2 software.

In case of problems, please read the [online BLAST help](#).
If your question is not covered, please contact [<helpdesk@expasy.org>](mailto:helpdesk@expasy.org).

NCBI BLAST program reference [PMID:9254694]:

Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W., Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. 25:3389-3402(1997).

Query length: 10 AA

Date run: 2004-04-30 22:33:09 UTC+0100 on sib-gml.unil.ch

Program: NCBI BLASTP 1.5.4-Paracel [2003-06-05]

Database: EXPASY/UniProt

1,459,789 sequences; 465,400,423 total letters

List of potentially matching sequences

Send selected sequences to

☐ Include query sequence

Db AC

Description

Score E-value

☐ tr [Q9ZLD5](#) Outer membrane protein/porin [HOPE] [Helicobacter pylo... 32 0.95

☐ tr [O25410](#) Outer membrane protein (OMP15) [HP0706] [Helicobacter ... 32 0.95

Graphical overview of the alignments

to resubmit your query after masking regions matching [PROSITE](#) profiles or [Pfam](#) HMMs

([?](#) Help) (use [ScanProsite](#) for more details about PROSITE matches)

Profile hits				
Pfam hits				
	Matches on query sequence			Mat
Submission	1			1
Q9ZLD5				
025410				
	1			
Submission				
Identity	0	25	50	75 100%

Alignments

tr Q9ZLD5 Outer membrane protein/porin [HOPE] [Helicobacter pylori J99] 270 AA
(Campylobacter pylori J99)]

align

Score = 32.0 bits (68), Expect = 0.95
Identities = 10/10 (100%), Positives = 10/10 (100%)

Query: 1 FVALGLLSAV 10
FVALGLLSAV
Sbjct: 4 FVALGLLSAV 13

tr O25410 Outer membrane protein (OMP15) [HP0706] [Helicobacter pylori] 273 AA
(Campylobacter pylori)]

align

Score = 32.0 bits (68), Expect = 0.95
Identities = 10/10 (100%), Positives = 10/10 (100%)

Query: 1 FVALGLLSAV 10
FVALGLLSAV
Sbjct: 7 FVALGLLSAV 16

Database: EXPASY/UniProt

Posted date: Apr 25, 2004 4:51 AM

Number of letters in database: 465,400,423

Number of sequences in database: 1,459,789

Lambda	K	H
0.342	0.301	1.60

Gapped		
Lambda	K	H
0.294	0.110	0.610

Matrix: PAM30

Gap Penalties: Existence: 9, Extension: 1
Number of HSP's successfully gapped in prelim test: 0
length of query: 10
length of database: 465,400,423
effective HSP length: 1
effective length of query: 9
effective length of database: 463,940,634
effective search space: 4175465706
effective search space used: 4175465706
T: 16
A: 40
X1: 15 (7.4 bits)
X2: 35 (14.8 bits)
X3: 58 (24.6 bits)
S1: 41 (22.0 bits)
S2: 61 (29.1 bits)

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ialog level 04.06.01D

Reconnected in file OS 30apr04 10:58:00

*
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* ALL NEW CURRENT YEAR RANGES HAVE BEEN * * *
* * * INSTALLED * * *
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File 155:MEDLINE(R) 1966-2004/Apr W4
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File 399:CA SEARCH(R) 1967-2004/UD=14018
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File 5:Biosis Previews(R) 1969-2004/Apr W4
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File 71:ELSEVIER BIOBASE 1994-2004/Apr W3
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File 654:US Pat.Full. 1976-2004/Apr 27
(c) Format only 2004 The Dialog Corp.
*File 654: US published applications now online. See HELP NEWS 654
for details. Reassignments current through December 2, 2003.
File 73:EMBASE 1974-2004/Apr W4
(c) 2004 Elsevier Science B.V.
File 349:PCT FULLTEXT 1979-2002/UB=20040415,UT=20040408
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(c) 2004 FSTA IFIS Publishing
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Set Items Description

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Cost is in DialUnits

?ds

Set Items Description

S1 67 (HELICOBACT? OR PYLORI OR PYLORIS OR PYLORIDIS) (3N) PORIN?

S2 27 RD (unique items)

?t s2/9/3

2/9/3 (Item 3 from file: 155)
DIALOG(R) File 155:MEDLINE(R)
(c) format only 2004 The Dialog Corp. All rts. reserv.

10652641 PMID: 10762234

Functional expression in Escherichia coli and membrane topology of porin HopE, a member of a large family of conserved proteins in Helicobacter pylori.

Bina J; Bains M; Hancock R E
Department of Microbiology, University of British Columbia, Vancouver,
British Columbia V6T 1Z3, Canada.

Journal of bacteriology (UNITED STATES) May 2000, 182 (9) p2370-5,
ISSN 0021-9193 Journal Code: 2985120R

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

HopE is one of the smallest members of a family of 31 outer membrane proteins in Helicobacter pylori and has been shown to function as a porin. In this study it was cloned into Escherichia coli where it was expressed in the outer membrane, as confirmed by indirect immunofluorescence using HopE-specific antibodies. HopE purified from E. coli reconstituted channels in planar bilayer membranes that were the same size as those formed by HopE purified from H. pylori. A model of the membrane topology of HopE was constructed and indicated that this protein formed a beta-barrel with 16 transmembrane amphipathic beta-strands. The accuracy of this model was tested by linker insertion mutagenesis, assuming that, like other porins, amino acid insertions were not tolerated in the transmembrane beta-strands but were tolerated in the adjoining loop regions. Generally, the results obtained with a series of 12 insertions of the sequence RSKDV and two substitutions were consistent with the topological model. The preponderance of amino acids that were conserved in the extended family of HopE paralogs were predicted to be within the membrane and comprised 45% of all residues in the membrane.

Tags: Support, Non-U.S. Gov't

Descriptors: Bacterial Proteins--metabolism--ME; *Escherichia coli
--metabolism--ME; * Helicobacter pylori --metabolism--ME; * Porins
--metabolism--ME; Amino Acid Sequence; Cloning, Molecular; Gene Expression;
Helicobacter pylori--genetics--GE; Models, Biological; Molecular Sequence
Data; Porins--genetics--GE

CAS Registry No.: 0 (Bacterial Proteins); 0 (Porins)

Record Date Created: 20000613

Record Date Completed: 20000613

?t s2/3,kwic/5 6 7 13 19 20 21 22

>>>KWIC option is not available in file(s): 398, 399

2/3,KWIC/5 (Item 1 from file: 440)
DIALOG(R) File 440:Current Contents Search(R)
(c) 2004 Inst for Sci Info. All rts. reserv.

13035941 References: 91

TITLE: Modification of host cell apoptosis by viral and bacterial pathogens

AUTHOR(S): Muller A (REPRINT); Rudel T

AUTHOR(S) E-MAIL: mueller@mpiib-erlin.mpg.de; rudel@mpiib-berlin.mpg.de

CORPORATE SOURCE: Max Planck Inst Infekt Biol, Mol Biol Abt, Schumannstr

21-22/D-10117 Berlin//Germany/ (REPRINT); Max Planck Inst Infekt Biol,

Mol Biol Abt, /D-10117 Berlin//Germany/

PUBLICATION TYPE: JOURNAL

PUBLICATION: INTERNATIONAL JOURNAL OF MEDICAL MICROBIOLOGY, 2001, V291, N3
(AUG), P197-207

GENUINE ARTICLE#: 469AN

PUBLISHER: URBAN & FISCHER VERLAG, BRANCH OFFICE JENA, P O BOX 100537,
D-07705 JENA, GERMANY

ISSN: 1438-4221

LANGUAGE: English DOCUMENT TYPE: REVIEW (ABSTRACT AVAILABLE)

...IDENTIFIERS--NF-KAPPA-B; CYTOCHROME-C RELEASE; ANION-SELECTIVE CHANNELS;
HELICOBACTER - PYLORI ; SHIGELLA-FLEXNERI; PORIN PORB;

YERSINIA-ENTEROCOLITICA; MACROPHAGE APOPTOSIS; DEATH RECEPTORS;
INFECTED-CELLS

2/3,KWIC/6 (Item 2 from file: 440)
DIALOG(R)File 440:Current Contents Search(R)
(c) 2004 Inst for Sci Info. All rts. reserv.

12618908 References: 27

TITLE: Characterization of proteins in the outer membrane preparation of a murine pathogen, Helicobacter bilis

AUTHOR(S): Ge ZM; Doig P; Fox JG (REPRINT)

AUTHOR(S) E-MAIL: jgfox@mit.edu

CORPORATE SOURCE: MIT, Div Comparat Med, 16-825,77 Massachusetts Ave/Cambridge//MA/02139 (REPRINT); MIT, Div Comparat Med, /Cambridge//MA/02139; AstraZeneca R&D Boston, /Waltham//MA/

PUBLICATION TYPE: JOURNAL

PUBLICATION: INFECTION AND IMMUNITY, 2001, V69, N5 (MAY), P3502-3506

GENUINE ARTICLE#: 423CT

PUBLISHER: AMER SOC MICROBIOLOGY, 1752 N ST NW, WASHINGTON, DC 20036-2904 USA

ISSN: 0019-9567

LANGUAGE: English DOCUMENT TYPE: ARTICLE (ABSTRACT AVAILABLE)

...IDENTIFIERS--GRAM-NEGATIVE BACTERIA; SCID MICE; BOWEL-DISEASE; PYLORI; PORIN; IDENTIFICATION; LOCALIZATION; SEQUENCE; ANTIGENS; ADHESION

2/3,KWIC/7 (Item 3 from file: 440)
DIALOG(R)File 440:Current Contents Search(R)
(c) 2004 Inst for Sci Info. All rts. reserv.

12555237 References: 29

TITLE: Characterization of four members of a multigene family encoding outer membrane proteins of Helicobacter pylori and their potential for vaccination

AUTHOR(S): Peck B; Ortkamp M; Nau U; Niederweis M; Hundt E; Knapp B (REPRINT)

AUTHOR(S) E-MAIL: Bernhard.Knapp@chiron-behring.com

CORPORATE SOURCE: Chiron Behring GmbH & Co, Preclin Res, /D-35006 Marburg//Germany/ (REPRINT); Chiron Behring GmbH & Co, Preclin Res, /D-35006 Marburg//Germany//; Univ Erlangen Nurnberg, Dept Microbiol, /D-91058 Erlangen//Germany/

PUBLICATION TYPE: JOURNAL

PUBLICATION: MICROBES AND INFECTION, 2001, V3, N3 (MAR), P171-179

GENUINE ARTICLE#: 415YX

PUBLISHER: EDITIONS SCIENTIFIQUES MEDICALES ELSEVIER, 23 RUE LINOIS, 75724 PARIS CEDEX 15, FRANCE

ISSN: 1286-4579

LANGUAGE: English DOCUMENT TYPE: ARTICLE (ABSTRACT AVAILABLE)

2/3,KWIC/13 (Item 3 from file: 398)
DIALOG(R)File 398:Chemsearch
(c) 2004 Amer.Chem.Soc. All rts. reserv.

CAS REGISTRY NUMBER: 489070-84-0

MOLECULAR FORMULA: Unknown

CA NAME(S):

HP=Outer membrane protein/porin (Helicobacter pylori strain J99 gene hope) (9CI)

SYNONYMS: GenBank AAD06223; GenBank AAD06223 (Translated from: GenBank AE001496)

2/3,KWIC/19 (Item 2 from file: 654)
DIALOG(R)File 654:US Pat.Full.
(c) Format only 2004 The Dialog Corp. All rts. reserv.

5580750 **IMAGE Available

Utility

Helicobacter pylori adhesin binding group antigen

Inventor: Boren, Thomas, Torelvagen 68 S-906 28, Umea, SE
Arnqvist, Anna, O. Brinkvagen 55 S-903, 21 Umea, SE
Hammarstrom, Lennart, Avd. for Klinisk Immunologi Huddinge
Sjukhus S-141, 86 Huddinge, SE
Normark, Staffan, Vallhallavagen 126 S-1141, 41 Stockholm, SE
Ilver, Dag, Bankgatan 18 S-902, 35 Umea, SE

Assignee: Unassigned

Examiner: Smith, Lynette R. F. (Art Unit: 165)

Assistant Examiner: Portner, Ginny Allen

Law Firm: Birch, Stewart, Kolasch & Birch, LLP

	Publication Number	Kind	Date	Application Number	Filing Date
Main Patent	US 6709656	A	20040323	US 99202178	19990210
PCT	WO 9747646		19971218	WO 97SE1009	19970610
		371:			
		102e:			
Priority				SE 962287	19960610
				SE 971014	19970319

Fulltext Word Count: 9027

Summary of the Invention:

...acid sequence of the purified BAB adhesin exhibit homologies to
outer membrane proteins of H. pylori porins .

2/3,KWIC/20 (Item 3 from file: 654)

DIALOG(R)File 654:US Pat.Full.

(c) Format only 2004 The Dialog Corp. All rts. reserv.

0005376656 **IMAGE Available

Derwent Accession: 2001-639461

Method for identifying helicobacter antigens

Inventor: Meyer, Thomas, INV
Jungblut, Peter, INV
Baumann, Dirk, INV
Aebischer, Anton, INV
Haas, Gaby, INV
Zimny-Arndt, Ursula, INV
Lamer, Stephanie, INV
Karaali, Galip, INV
Sabarth, Nicolas, INV
Wendland, Meike, INV

Correspondence Address: ROTHWELL, FIGG, ERNST & MANBECK, P.C., 1425 K
STREET, N.W. SUITE 800, WASHINGTON, DC, 20005, US

	Publication Number	Kind	Date	Application Number	Filing Date
Main Patent	US 20030180330	A1	20030925	US 2003257976	20030429
PCT				WO 2001EP4728	20010426
Priority				EP 2000108968	20000427
				EP 2001101439	20010123

Fulltext Word Count: 25092

Description of the Invention:

...up to 800 Dalton have been reported for some porins (Benz and Bauer,
1988). H. pylori might also posses porins with such a large exclusion
limit and in this case, the biotinylation reagent (molecular weight...

2/3,KWIC/21 (Item 4 from file: 654)
DIALOG(R)File 654:US Pat.Full.
(c) Format only 2004 The Dialog Corp. All rts. reserv.

4704307 **IMAGE Available
Derwent Accession: 1998-052240
Utility
REASSIGNED

C/ Blood group antigen binding protein and corresponding agents
; NUCLEOTIDE SEQUENCES CODING ADHESIN FOR USE IN THE TREATMENT OF
GASTROINTESTINAL DISORDERS AND PEPTIC ULCERS

Inventor: Boren, Thomas, Torelv.ang.gen 68, S-906 28 Ume.ang., SE
Arngvist, Anna, Ume.ang., SE
Normark, Staffan, Stockholm, SE
Ilver, Dag, Ume.ang., SE

Assignee: Boren, Thomas (05), Umea, SE
Unassigned Or Assigned To Individual (Code: 68000)

Examiner: Smith, Lynette R. F. (Art Unit: 165)

Assistant Examiner: Portner, Ginny Allen

Law Firm: Birch, Stewart, Kolasch & Birch, LLP

	Publication Number	Kind	Date	Application Number	Filing Date
Main Patent	US 6410719	A	20020625	US 9821560	19980210
Continuation	Pending			WO 97SE1009	19970610
Priority				SE 962287	19960610
				SE 971014	19970319

Fulltext Word Count: 4725

Summary of the Invention:

...acid sequence of the purified BAB adhesin exhibit homologies to
outer membrane proteins of H. pylori porins .

2/3,KWIC/22 (Item 1 from file: 349)
DIALOG(R)File 349:PCT FULLTEXT
(c) 2004 WIPO/Univentio. All rts. reserv.

00558762

i(HELICOBACTER PYLORI) VACCINE
VACCIN ANTI-i(HELICOBACTER PILORI)

Patent Applicant/Assignee:

CHIRON BEHRING GMBH & CO,
KNAPP Bernhard,
DIEHL Klaus-Dieter,
HUNDT Erika,

Inventor(s):

KNAPP Bernhard,
DIEHL Klaus-Dieter,
HUNDT Erika,

Patent and Priority Information (Country, Number, Date):

Patent: WO 200022135 A1 20000420 (WO 0022135)

Application: WO 99EP7754 19991014 (PCT/WO EP9907754)

Priority Application: DE 19847628 19981015

Designated States: CA JP US AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL
PT SE

Publication Language: German

Fulltext Word Count: 8903

Fulltext Availability:

Detailed Description

Detailed Description

... induzieren, die die bakterielle Adhäsion an der mukosalen Oberfläche
verhindern. Ausserdem verfügt die äussere Membran von Helicobacter

pylori uber Porine mit Molekulargewichten von 30 kD (Tufano et al. (1
994>>, 48 kD, 49 kDy 50...

?logoff hold

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30apr04 10:58:08 User228206 Session D2159.4
$0.03      0.010 DialUnits File155
$0.21      1 Type(s) in Format 9
$0.21      1 Types
$0.24      Estimated cost File155
$0.97      0.046 DialUnits File440
$17.40     3 Type(s) in Format 3
$17.40     3 Types
$18.37     Estimated cost File440
$0.06      0.005 DialUnits File399
$0.06      Estimated cost File399
$0.16      0.005 DialUnits File398
$10.80     1 Type(s) in Format 3
$10.80     1 Types
$10.96     Estimated cost File398
$0.10      0.005 DialUnits File34
$0.10      Estimated cost File34
$0.03      0.005 DialUnits File5
$0.03      Estimated cost File5
$0.04      0.005 DialUnits File71
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$1.35      0.229 DialUnits File654
$2.10      3 Type(s) in Format 3
$2.10      3 Types
$3.45      Estimated cost File654
$0.05      0.005 DialUnits File73
$0.05      Estimated cost File73
$0.19      0.041 DialUnits File349
$1.60      1 Type(s) in Format 3
$1.60      1 Types
$1.79      Estimated cost File349
$0.01      0.005 DialUnits File98
$0.01      Estimated cost File98
$0.02      0.005 DialUnits File144
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$0.02      Estimated cost File35
$0.02      0.005 DialUnits File51
$0.02      Estimated cost File51
$0.01      0.005 DialUnits File143
$0.01      Estimated cost File143
$0.03      0.005 DialUnits File156
$0.03      Estimated cost File156
$0.10      0.005 DialUnits File357
$0.10      Estimated cost File357
$0.02      0.005 DialUnits File444
$0.02      Estimated cost File444
$0.02      0.005 DialUnits File484
$0.02      Estimated cost File484
OneSearch, 19 files, 0.402 DialUnits FileOS
$0.24      TELNET
$35.58     Estimated cost this search
$35.58     Estimated total session cost 0.402 DialUnits
```

Status: Signed Off. (1 minutes)

10652641 PMID: 10762234

Functional expression in Escherichia coli and membrane topology of porin HopE, a member of a large family of conserved proteins in Helicobacter pylori.

Bina J; Bains M; Hancock R E

Department of Microbiology, University of British Columbia, Vancouver, British Columbia V6T 1Z3, Canada.

Journal of bacteriology (UNITED STATES) May 2000, 182 (9) p2370-5, ISSN 0021-9193 Journal Code: 2985120R

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

HopE is one of the smallest members of a family of 31 outer membrane proteins in Helicobacter pylori and has been shown to function as a porin. In this study it was cloned into Escherichia coli where it was expressed in the outer membrane, as confirmed by indirect immunofluorescence using HopE-specific antibodies. HopE purified from E. coli reconstituted channels in planar bilayer membranes that were the same size as those formed by HopE purified from H. pylori. A model of the membrane topology of HopE was constructed and indicated that this protein formed a beta-barrel with 16 transmembrane amphipathic beta-strands. The accuracy of this model was tested by linker insertion mutagenesis, assuming that, like other porins, amino acid insertions were not tolerated in the transmembrane beta-strands but were tolerated in the adjoining loop regions. Generally, the results obtained with a series of 12 insertions of the sequence RSKDV and two substitutions were consistent with the topological model. The preponderance of amino acids that were conserved in the extended family of HopE paralogs were predicted to be within the membrane and comprised 45% of all residues in the membrane.

Tags: Support, Non-U.S. Gov't

Descriptors: Bacterial Proteins--metabolism--ME; *Escherichia coli --metabolism--ME; * Helicobacter pylori --metabolism--ME; * Porins --metabolism--ME; Amino Acid Sequence; Cloning, Molecular; Gene Expression; Helicobacter pylori--genetics--GE; Models, Biological; Molecular Sequence Data; Porins--genetics--GE

CAS Registry No.: 0 (Bacterial Proteins); 0 (Porins)

Record Date Created: 20000613

Record Date Completed: 20000613

7/6,KWIC/40 (Item 1 from file: 5)
DIALOG(R)File 5:(c) 2004 BIOSIS. All rts. reserv.

0009492540 BIOSIS NO.: 199497513825

Identification of surface-exposed outer membrane antigens of *Helicobacter pylori*
1994

Identification of surface-exposed outer membrane antigens of *Helicobacter pylori*

...ABSTRACT: the potential significance of surface-localized antigens in the colonization by and disease processes of *Helicobacter pylori*, few such components have been unequivocally identified and/or characterized. To further investigate the...

...H. pylori. Both the 51- and 48-kDa antigens were heat modifiable and likely are **porins**. A conserved 31-kDa protein may represent another species of **porin**. A method involving sucrose density ultracentrifugation and Triton extraction that allows the preparation of H...

...of the H. pylori outer membrane is similar structurally to those of other species of *Helicobacter* but markedly different from those of taxonomically related *Campylobacter* spp. and *Escherichia coli*. H. pylori ...

7/6,KWIC/41 (Item 2 from file: 5)
DIALOG(R)File 5:(c) 2004 BIOSIS. All rts. reserv.

0009322545 BIOSIS NO.: 199497343830

Isolation and characterization of a family of **porin proteins** from *Helicobacter pylori*
1994

Isolation and characterization of a family of **porin proteins** from *Helicobacter pylori*

DESCRIPTORS:

...ORGANISMS: *Helicobacter pylori* (Aerobic Helical or Vibrioid Gram-Negatives)

7/6,KWIC/42 (Item 3 from file: 5)
DIALOG(R)File 5:(c) 2004 BIOSIS. All rts. reserv.

0009202729 BIOSIS NO.: 199497224014

Immunobiological activities of *Helicobacter pylori* **porins**
1994

Immunobiological activities of *Helicobacter pylori* **porins**

ABSTRACT: Studies were carried out on some biological activities of *Helicobacter pylori* **porins** in vitro. We extracted and purified a **porin** with an apparent molecular mass of 30 kDa. Human polymorphonuclear leukocytes preincubated with H. pylori **porins** showed a decrease of chemotaxis, of adherence to nylon wool, and of chemiluminescence. Used as chemotaxins in place of zymosan-activated serum or as chemotaxinogens in place of zymosan, the **porins** induced polymorphonuclear leukocyte migration. Human monocytes and lymphocytes cultivated in the presence of H. pylori **porins** released cytokines. Release of the various cytokines studied was obtained with differentiated kinetics and at various **porin** concentrations. Starting only 3 h after culture, tumor necrosis factor alpha is released quickly, reaching a peak at 18 h, at a **porin** concentration of 1 μ -g/ml/ 10^{-6} cells. Interleukin-6 (IL-6) appears later ...

...is released after 6 h of culture, with a peak at 24 h, at a **porin** concentration of 10 μ -g/ml/ 10^{-6} cells. Lymphocytes stimulated by H. pylori **porins** release gamma interferon after 18 h of culture at higher

concentrations of **porins** (20 mu-g/ml/10⁻⁶ cells). Granulocyte macrophage colony-stimulating factor is released from...

...both IL-3 and IL-4 are released after 18 h of culture at different **porin** concentrations (0.1 and 1 mu-g/ml/10⁻⁶ cells, respectively). Our results lead us to think that during *H. pylori* infection, surface components, **porins** in particular, are able to induce a series of chain reactions ranging from the inflammatory...

DESCRIPTORS:

...ORGANISMS: **Helicobacter pylori** (Aerobic Helical or Vibrioid Gram-Negatives

7/6,KWIC/43 (Item 4 from file: 5)

DIALOG(R)File 5:(c) 2004 BIOSIS. All rts. reserv.

0008956472 BIOSIS NO.: 199396120888

Mechanisms of quinolone resistance in clinical isolates: Accumulation of sparfloxacin and of fluoroquinolones of various hydrophobicity, and analysis of membrane composition

1993

...ABSTRACT: in the uptake of quinolones by bacterial cells, and provided evidence that sparfloxacin used both **porin** and the self-promoted uptake pathway for its uptake.

DESCRIPTORS:

ORGANISMS: **Helicobacter pylori** (Aerobic Helical or Vibrioid Gram-Negatives...

7/6,KWIC/44 (Item 5 from file: 5)

DIALOG(R)File 5:(c) 2004 BIOSIS. All rts. reserv.

0008932175 BIOSIS NO.: 199396096591

In vitro susceptibility of Helicobacter pylori to trospectomycin, pirlimycin (U-57930E), mirincamycin (U-24729A) and N-demethylclindamycin (U-26767A)

1993

In vitro susceptibility of Helicobacter pylori to trospectomycin, pirlimycin (U-57930E), mirincamycin (U-24729A) and N-demethylclindamycin (U-26767A)

...ABSTRACT: of trospectomycin, pirlimycin, mirincamycin and N-demethyl clindamycin was measured against 46 clinical isolates of **Helicobacter pylori** using an agar dilution technique. The MIC50 and MIC90 were 4 and 64 mu...

...were sensitive to trospectomycin, this drug may be useful in treating infection with metronidazole resistant **Helicobacter pylori**.

DESCRIPTORS:

MISCELLANEOUS TERMS: ... **PORIN** ;

7/6,KWIC/45 (Item 1 from file: 34)

DIALOG(R)File 34:(c) 2004 Inst for Sci Info. All rts. reserv.

03491861 Genuine Article#: PH298 Number of References: 48

Title: IDENTIFICATION OF SURFACE-EXPOSED OUTER-MEMBRANE ANTIGENS OF HELICOBACTER -PYLORI (Abstract Available)

Title: IDENTIFICATION OF SURFACE-EXPOSED OUTER-MEMBRANE ANTIGENS OF HELICOBACTER -PYLORI

...Abstract: the potential significance of surface-localized antigens in the colonization by and disease processes of **Helicobacter pylori**, few such components have been unequivocally identified and/or characterized. To further investigate the...

...*H. pylori*. Both the 51 and 48-kDa antigens were heat modifiable and

likely are **porins** . A conserved 31-kDa protein may represent another species of **porin** . A method involving sucrose density ultracentrifugation and Triton extraction that allows the preparation of H...

...of the H. pylori outer membrane is similar structurally to those of other species of **Helicobacter** but markedly different from those of taxonomically related Campylobacter spp. and Escherichia coli. H. pylori...

...Research Fronts: 3056 002 (UPTAKE OF SURFACTANT PROTEIN-B; CASEIN KINASE-II; CATALYTIC SUBUNITS)
92-2733 001 (**HELICOBACTER** -PYLORI INFECTION; TREATMENT OF PEPTIC-ULCER DISEASE; GASTRITIS IN HEALTHY-SUBJECTS)
92-6495 001 (LIPOPOLYSACCHARIDE...

7/6,KWIC/46 (Item 2 from file: 34)
DIALOG(R)File 34:(c) 2004 Inst for Sci Info. All rts. reserv.

03094853 Genuine Article#: NC074 Number of References: 47
Title: **IMMUNOBIOLOGICAL ACTIVITIES OF HELICOBACTER -PYLORI PORINS** (Abstract Available)

Title: **IMMUNOBIOLOGICAL ACTIVITIES OF HELICOBACTER -PYLORI PORINS**
Abstract: Studies were carried out on some biological activities of **Helicobacter pylori porins** in vitro. We extracted and purified a **porin** with an apparent molecular mass of 30 kDa. Human polymorphonuclear leukocytes preincubated with H. pylori **porins** showed a decrease of chemotaxis, of adherence to nylon wool, and of chemiluminescence. Used as chemotaxins in place of zymosan-activated serum or as chemotaxinogens in place of zymosan, the **porins** induced polymorphonuclear leukocyte migration. Human monocytes and lymphocytes cultivated in the presence of H. pylori **porins** released cytokines. Release of the various cytokines studied was obtained with differentiated kinetics and at various **porin** concentrations. Starting only 3 h after culture, tumor necrosis factor alpha is released quickly, reaching a peak at 18 h, at a **porin** concentration of 1 mu g/ml/10(6) cells). Interleukin-6 (IL 6) appears later...

...is released after 6 h of culture, with a peak at 24 h, at a **porin** concentration of 10 mu g/ml/10(6) cells. Lymphocytes stimulated by H. pylori **porins** release gamma interferon after 18 h of culture at higher concentrations of **porins** (20 mu g/ml/10(6) cells). Granulocyte macrophage colony-stimulating factor is released from...

...both IL-3 and IL-4 are released after 18 h of culture at different **porin** concentrations (0.1 and 1 mu g/ml/10(6) cells, respectively). Our results lead us to think that during H. pylori infection, surface components, **porins** in particular, are able to induce a series of chain reactions ranging from the inflammatory...

...Identifiers--HUMAN POLYMORPHONUCLEAR LEUKOCYTES; SALMONELLA-TYPHIMURIUM **PORINS** ; ACTIVATING-FACTOR SYNTHESIS; OUTER-MEMBRANE PROTEINS; GROWTH-FACTOR ACTIVITY; ESCHERICHIA-COLI; BIOLOGICAL-ACTIVITIES; LIPOPOLYSACCHARIDE; CELLS...

Research Fronts: 92-2733 002 (**HELICOBACTER** -PYLORI INFECTION; TREATMENT OF PEPTIC-ULCER DISEASE; GASTRITIS IN HEALTHY-SUBJECTS)
92-1291 001 (SERUM...

...92-7442 001 (OUTER-MEMBRANE PROTEIN; GENE IN SALMONELLA-TYPHIMURIUM; GRAM-NEGATIVE BACTERIA; ESCHERICHIA-COLI **PORIN** CHANNELS; SSC PERMEABILITY MUTANT; NULL MUTATIONS)

7/6,KWIC/47 (Item 3 from file: 34)
DIALOG(R)File 34:(c) 2004 Inst for Sci Info. All rts. reserv.

02171547 Genuine Article#: KG501 Number of References: 46
Title: **PROTEUS-MIRABILIS UREASE - TRANSCRIPTIONAL REGULATION BY URER** (Abstract Available)

...Abstract: number of DNA-binding proteins, including E. coli proteins that regulate acid phosphatase synthesis (AppY), **porin** synthesis (EnvY), and rhamnose utilization (RhaR). These data suggest that UreR governs the inducibility of...

Research Fronts: 91-2242 002 (**HELICOBACTER** -PYLORI INFECTION; HISTOLOGIC GASTRITIS IN ASYMPTOMATIC HISPANICS; ASSOCIATED GASTRODUODENAL DISEASES)
91-4817 002 (LIPASE GENE...

7/6,KWIC/48 (Item 4 from file: 34)
DIALOG(R)File 34:(c) 2004 Inst for Sci Info. All rts. reserv.

02130672 Genuine Article#: KD035 Number of References: 20
Title: IMMUNOLOGICAL CROSS-REACTIVITY BETWEEN OUTER-MEMBRANE PORE PROTEINS OF CAMPYLOBACTER-JEJUNI AND ESCHERICHIA-COLI (Abstract Available)

Abstract: Immunocrossreactivity between the major outer membrane protein (MOMP) of Campylobacter jejuni 85H and the OmpC **porin** of Escherichia coli K-12 was observed. These results indicate that a common antigenic domain...

...degrees-C treatment suggesting that it is buried in the native conformation of the respective **porins**. In addition, differences were observed between the major outer membrane proteins from various C. jejuni...

...jejuni pathogenic strains tested contained a protein exhibiting a similar electrophoretic profile to the 85H **porin**.
Research Fronts: 90-2234 001 (**HELICOBACTER** -PYLORI INFECTION; CHRONIC GASTRITIS; PEPTIC-ULCER DISEASE)
90-2781 001 (THERMOPHILIC CAMPYLOBACTERS; SOIL SAMPLES; UNITED...

7/6,KWIC/49 (Item 5 from file: 34)
DIALOG(R)File 34:(c) 2004 Inst for Sci Info. All rts. reserv.

01530712 Genuine Article#: HG540 Number of References: 21
Title: EXTRACTION AND BIOCHEMICAL ANALYSES OF HELICOBACTER -PYLORI LIPOPOLYSACCHARIDES (Abstract Available)

Title: EXTRACTION AND BIOCHEMICAL ANALYSES OF HELICOBACTER -PYLORI LIPOPOLYSACCHARIDES

Abstract: Lipopolysaccharides were isolated from dehydrated **Helicobacter pylori** cells by the phenol-chloroform-petroleum ether and hot phenol/water extraction techniques. Biochemical...

...Research Fronts: NATIVE PROTEINS; SERUM RESISTANCE; BACTERICIDAL ACTIVITY)
90-7846 001 (OUTER-MEMBRANE PERMEABILITY; ESCHERICHIA-COLI MUTANTS; **PORIN** PROTEINS; HAEMOPHILUS-INFLUENZAE TYPE-B; GRAM-NEGATIVE CELL-ENVELOPE)

7/6,KWIC/50 (Item 1 from file: 71)
DIALOG(R)File 71:(c) 2004 Elsevier Science B.V. All rts. reserv.

00156154 94157553
Identification of surface-exposed outer membrane antigens of Helicobacter pylori
PUBLICATION DATE: 19940000

Identification of surface-exposed outer membrane antigens of Helicobacter pylori

...the potential significance of surface-localized antigens in the colonization by and disease processes of **Helicobacter pylori**, few such components have been unequivocally identified and/or characterized. To further investigate the...

...H. pylori. Both the 51- and 48-kDa antigens were heat modifiable and likely are **porins**. A conserved 31-kDa protein may represent another species of **porin**. A method involving sucrose density ultracentrifugation and Triton extraction that allows the preparation of H...

...of the H. pylori outer membrane is similar structurally to those of other species of **Helicobacter** but markedly different from those of taxonomically related *Campylobacter* spp. and *Escherichia coli*. H. pylori...

7/6,KWIC/51 (Item 2 from file: 71)
DIALOG(R)File 71:(c) 2004 Elsevier Science B.V. All rts. reserv.

00101686 94074752
Immunobiological activities of Helicobacter pylori porins
PUBLICATION DATE: 19940000

Immunobiological activities of Helicobacter pylori porins

Studies were carried out on some biological activities of **Helicobacter pylori porins** in vitro. We extracted and purified a **porin** with an apparent molecular mass of 30 kDa. Human polymorphonuclear leukocytes preincubated with H. pylori **porins** showed a decrease of chemotaxis, of adherence to nylon wool, and of chemiluminescence. Used as chemotaxins in place of zymosan- activated serum or as chemotaxinogens in place of zymosan, the **porins** induced polymorphonuclear leukocyte migration. Human monocytes and lymphocytes cultivated in the presence of H. pylori **porins** released cytokines. Release of the various cytokines studied was obtained with differentiated kinetics and at various **porin** concentrations. Starting only 3 h after culture, tumor necrosis factor alpha is released quickly, reaching a peak at 18 h, at a **porin** concentration of 1 mug/ml/10sup 6 cells. Interleukin-6 (IL-6) appears later, with...

...is released after 6 h of culture, with a peak at 24 h, at a **porin** concentration of 10 mug/ml/10sup 6 cells. Lymphocytes stimulated by H. pylori **porins** release gamma interferon after 18 h of culture at higher concentrations of **porins** (20 mug/ml/10sup 6 cells). Granulocyte macrophage colony-stimulating factor is released from 6...

...both IL-3 and IL-4 are released after 18 h of culture at different **porin** concentrations (0.1 and 1 mug/ml/10sup 6 cells, respectively). Our results lead us to think that during H. pylori infection, surface components, **porins** in particular, are able to induce a series of chain reactions ranging from the inflammatory...

7/6,KWIC/52 (Item 1 from file: 73)
DIALOG(R)File 73:(c) 2004 Elsevier Science B.V. All rts. reserv.

05893045 EMBASE No: 1994299275
Identification of surface-exposed outer membrane antigens of Helicobacter pylori
1994

Identification of surface-exposed outer membrane antigens of Helicobacter pylori

...the potential significance of surface-localized antigens in the colonization by and disease processes of **Helicobacter pylori**, few such components have been unequivocally identified and/or characterized. To further investigate the...

...H. pylori. Both the 51- and 48-kDa antigens were heat modifiable and likely are **porins**. A conserved 31-kDa protein may represent another species of **porin**. A method involving sucrose density ultracentrifugation and Triton extraction that allows the preparation of H...

...of the H. pylori outer membrane is similar structurally to those of

other species of **Helicobacter** but markedly different from those of taxonomically related *Campylobacter* spp. and *Escherichia coli*. *H. pylori*...

MEDICAL DESCRIPTORS:

* **helicobacter** pylori; *stomach cancer

EMTREE CODES:

B3.80.40 ; C2.220.230.210.820; C2.220.230.820.820; C2.220.800...

7/6,KWIC/53 (Item 2 from file: 73)

DIALOG(R)File 73:(c) 2004 Elsevier Science B.V. All rts. reserv.

05704236 EMBASE No: 1994102224

Immunobiological activities of Helicobacter pylori porins
1994

Immunobiological activities of Helicobacter pylori porins

Studies were carried out on some biological activities of **Helicobacter pylori porins** in vitro. We extracted and purified a **porin** with an apparent molecular mass of 30 kDa. Human polymorphonuclear leukocytes preincubated with *H. pylori porins* showed a decrease of chemotaxis, of adherence to nylon wool, and of chemiluminescence. Used as chemotaxins in place of zymosan-activated serum or as chemotaxinogens in place of zymosan, the **porins** induced polymorphonuclear leukocyte migration. Human monocytes and lymphocytes cultivated in the presence of *H. pylori porins* released cytokines. Release of the various cytokines studied was obtained with differentiated kinetics and at various **porin** concentrations. Starting only 3 h after culture, tumor necrosis factor alpha is released quickly, reaching a peak at 18 h, at a **porin** concentration of 1 mug/ml/10sup 6 cells. Interleukin-6 (IL-6) appears later, with...

...is released after 6 h of culture, with a peak at 24 h, at a **porin** concentration of 10 mug/ml/10sup 6 cells. Lymphocytes stimulated by *H. pylori porins* release gamma interferon after 18 h of culture at higher concentrations of **porins** (20 mug/ml/10sup 6 cells). Granulocyte macrophage colony-stimulating factor is released from 6...

...both IL-3 and IL-4 are released after 18 h of culture at different **porin** concentrations (0.1 and 1 mug/ml/10sup 6 cells, respectively). Our results lead us to think that during *H. pylori* infection, surface components, **porins** in particular, are able to induce a series of chain reactions ranging from the inflammatory...

DRUG DESCRIPTORS:

* **porin**

MEDICAL DESCRIPTORS:

* **helicobacter** pylori; *immune response; *protein analysis

EMTREE CODES:

B3.80.40 ; G2.440.440; E1.50.150.710; J1.100; G1.560.90; E1...

7/6,KWIC/54 (Item 1 from file: 144)

DIALOG(R)File 144:(c) 2004 INIST/CNRS. All rts. reserv.

11563187 PASCAL No.: 94-0446530

Immunobiological activities of Helicobacter pylori porins
1994

Immunobiological activities of Helicobacter pylori porins

Studies were carried out on some biological activities of **Helicobacter pylori porins** in vitro. We extracted and purified a **porin** with an apparent molecular mass of 30 kDa. Human polymorphonuclear leukocytes preincubated with *H. pylori porins* showed a decrease of chemotaxis, of adherence to nylon wool, and of chemiluminescence. Used as chemotaxins in place of zymosan-activated serum or as chemotaxinogens in place of zymosan, the **porins** induced polymorphonuclear leukocyte migration. Human monocytes and lymphocytes cultivated in the presence of *H. pylori porins* released cytokines. Release of the various cytokines studied was obtained with differentiated kinetics and at various **porin** concentrations

English Descriptors: **Helicobacter** pylori; Human; **Porin** ; Granulocyte; Neutrophil; Lymphocyte; Monocyte; Adhesion; Chemotaxis; Chemiluminescence ; Cytokine; Release; Kinetics; Immunostimulation; Immunomodulation; Host agent relation...

French Descriptors: **Helicobacter** pylori; Homme; **Porine** ; Granulocyte; Neutrophile; Lymphocyte; Monocyte; Adherence; Chimiotactisme; Chimiluminescence; Cytokine; Liberation; Cinetique; Immunostimulation; Immunomodulation; Relation hote agent...

Spanish Descriptors: **Helicobacter** pylori; Hombre; **Porina** ; Granulocito; Neutrofilo; Linfocito; Monocito; Adherencia; Quimiotactismo; Quimioluminiscencia; Citoquina; Liberacion; Cinetica; Inmunoestimulacion; Inmunomodulacion; Relacion huesped agente...

7/6,KWIC/55 (Item 1 from file: 149)
DIALOG(R) File 149:(c) 2004 The Gale Group. All rts. reserv.

01235649 SUPPLIER NUMBER: 08864381 (USE FORMAT 7 OR 9 FOR FULL TEXT)
Lab tests: three decades of wonders. (includes related articles on imaging, and quality in physician office labs)
1990
WORD COUNT: 4575 LINE COUNT: 00373

... managers of clinical chemistry labs were shopping for glassware and rubber tubing. Today, they're **poring** over glossy brochures hyping fully automated machines that handle 40 patient samples at a time...

...unheard of in 1960, not to mention in Pasteur's time. The human immunodeficiency virus, **Helicobacter** pylori (formerly Campylobacter pylori), and Yersinia bacteria are all part of a day's work...

7/6,KWIC/56 (Item 1 from file: 159)
DIALOG(R) File 159:(c) format only 2002 Dialog Corporation. All rts. reserv.

02071892 94178947 PMID: 8132346
Immunobiological activities of Helicobacter pylori porins .
Apr 1994

Immunobiological activities of Helicobacter pylori porins .
Studies were carried out on some biological activities of **Helicobacter pylori porins** in vitro. We extracted and purified a **porin** with an apparent molecular mass of 30 kDa. Human polymorphonuclear leukocytes preincubated with H. pylori **porins** showed a decrease of chemotaxis, of adherence to nylon wool, and of chemiluminescence. Used as chemotaxins in place of zymosan-activated serum or as chemotaxinogens in place of zymosan, the **porins** induced polymorphonuclear leukocyte migration. Human monocytes and lymphocytes cultivated in the presence of H. pylori **porins** released cytokines. Release of the various cytokines studied was obtained with differentiated kinetics and at various **porin** concentrations. Starting only 3 h after culture, tumor necrosis factor alpha is released quickly, reaching a peak at 18 h, at a **porin** concentration of 1 microgram/ml/10(6) cells. Interleukin-6 (IL-6) appears later, with...

...is released after 6 h of culture, with a peak at 24 h, at a **porin** concentration of 10 micrograms/ml/10(6) cells, while IL-8 is released after 6 h of culture, with a peak at 24 h, at a **porin** concentration of 10 micrograms/ml/10(6) cells. Lymphocytes stimulated by H. pylori **porins** release gamma interferon after 18 h of culture at higher concentrations of **porins** (20 micrograms/ml/10(6) cells). Granulocyte macrophage colony-stimulating factor is released from 6...

...both IL-3 and IL-4 are released after 18 h of culture at different **porin** concentrations (0.1 and 1 microgram/ml/10(6) cells, respectively). Our results lead us to think that during H. pylori infection, surface components, **porins** in particular, are able to induce a series of chain reactions ranging from the inflammatory...

Major Descriptors: **Helicobacter pylori**--pathogenicity--PY; * **Porins**
--pharmacology--PD

Chemical Name: Interleukins; **Porins** ; Tumor Necrosis Factor;
Granulocyte-Macrophage Colony-Stimulating Factor

7/6,KWIC/57 (Item 2 from file: 159)

DIALOG(R)File 159:(c) format only 2002 Dialog Corporation. All rts. reserv.

01958044 93014165 PMID: 1328059

Immunochemical and biological characterization of outer membrane proteins of Porphyromonas endodontalis.

Nov 1992

... artificial liposomes composed of egg yolk phosphatidylcholine and dicetylphosphate, indicating that OMP-I exhibited significant **porin** activity. However, the liposomes containing heat-denatured OMP-I were scarcely active. Spontaneous and antigen...

Major Descriptors: Antibodies, Bacterial--immunology--IM; *Bacterial Outer Membrane Proteins--immunology--IM; * **Gram-Negative Bacteria** --immunology--IM; *Periapical Abscess--microbiology--MI

Minor Descriptors: Bacterial Outer Membrane Proteins --isolation and purification--IP; **Gram-Negative Bacteria** --chemistry--CH; Leukocytes, Mononuclear--immunology--IM; Lipopolysaccharides--chemistry--CH; Lipopolysaccharides--immunology--IM; Periapical Granuloma--immunology--IM; **Porins** ; Radicular Cyst--immunology--IM

Chemical Name: Antibodies, Bacterial; Bacterial Outer Membrane Proteins; Lipopolysaccharides; **Porins**

7/6,KWIC/58 (Item 1 from file: 399)

DIALOG(R)File 399:(c) 2004 American Chemical Society. All rts. reserv.

Identification of surface-exposed outer membrane antigens of Helicobacter pylori

7/6,KWIC/59 (Item 2 from file: 399)

DIALOG(R)File 399:(c) 2004 American Chemical Society. All rts. reserv.

Immunobiological activities of Helicobacter pylori porins

?logoff hold

30apr04 07:28:51 User228206 Session D2157.4

\$1.96 0.612 DialUnits File155

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\$0.80 5 Types

\$3.09 Estimated cost File5

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\$1.80 5 Types

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\$0.35 Estimated cost File48

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\$1.81 Estimated cost File65

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\$2.23 Estimated cost File71

\$2.75 0.281 DialUnits File73

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\$0.64 2 Types

\$3.39 Estimated cost File73

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\$0.59	Estimated cost File94			
	\$0.18	0.074	DialUnits	File98
\$0.18	Estimated cost File98			
	\$0.24	0.045	DialUnits	File135
\$0.24	Estimated cost File135			
	\$1.00	0.284	DialUnits	File144
	\$0.21	1	Type(s)	in Format 95 (KWIC)
	\$0.21	1	Types	
\$1.21	Estimated cost File144			
	\$0.39	0.089	DialUnits	File149
	\$0.26	1	Type(s)	in Format 95 (KWIC)
	\$0.26	1	Types	
\$0.65	Estimated cost File149			
	\$1.21	0.227	DialUnits	File156
\$1.21	Estimated cost File156			
	\$0.39	0.132	DialUnits	File159
	\$0.10	2	Type(s)	in Format 95 (KWIC)
	\$0.10	2	Types	
\$0.49	Estimated cost File159			
	\$0.36	0.080	DialUnits	File162
\$0.36	Estimated cost File162			
	\$0.14	0.041	DialUnits	File164
\$0.14	Estimated cost File164			
	\$0.51	0.052	DialUnits	File172
\$0.51	Estimated cost File172			
	\$0.10	0.030	DialUnits	File266
\$0.10	Estimated cost File266			
	\$0.13	0.037	DialUnits	File369
\$0.13	Estimated cost File369			
	\$0.17	0.048	DialUnits	File370
\$0.17	Estimated cost File370			
	\$5.27	0.420	DialUnits	File399
	\$1.10	2	Type(s)	in Format 6
	\$1.10	2	Types	
\$6.37	Estimated cost File399			
	\$0.76	0.037	DialUnits	File434
\$0.76	Estimated cost File434			
	\$0.17	0.035	DialUnits	File444
\$0.17	Estimated cost File444			
	\$0.20	0.032	DialUnits	File467
\$0.20	Estimated cost File467			
	OneSearch, 26 files, 4.513 DialUnits FileOS			
\$0.99	TELNET			
\$40.97	Estimated cost this search			
\$41.50	Estimated total session cost 4.678 DialUnits			

Status: Signed Off. (4 minutes)

Q9R4J2

31 kDa major NONSELECTIVE porin protein (Fragment) - Helicobacter pylori (Campylobacter pylori)

Q9R4R3

HOPD porin (Fragment) - Helicobacter pylori (Campylobacter pylori)

Q9R4R4

HOPC porin (Fragment) - Helicobacter pylori (Campylobacter pylori)

Q9R4R5

HOPB porin (Fragment) - Helicobacter pylori (Campylobacter pylori)

Q9R4R6

HOPA porin (Fragment) - Helicobacter pylori (Campylobacter pylori)

Q9ZKT6

Outer membrane protein/porin {GENE:HOPB OR JHP0849} - Helicobacter pylori J99 (Campylobacter pylori J99)

Q9ZKT7

Outer membrane protein/porin {GENE:HOPC OR JHP0848} - Helicobacter pylori J99 (Campylobacter pylori J99)

Q9ZLD5

Outer membrane protein/porin {GENE:HOPE OR JHP0645} - Helicobacter pylori J99 (Campylobacter pylori J99)

Q9ZMK5

Outer membrane protein/porin {GENE:HOPA OR JHP0214} - Helicobacter pylori J99 (Campylobacter pylori J99)

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Search		Swiss-Prot/TrEMBL		<input type="button" value="v"/>	for		<input type="text"/>	<input type="button" value="Go"/> <input type="button" value="Clear"/>

Search in Swiss-Prot and TrEMBL for: porin pylori

Swiss-Prot Release 43.2 of 26-Apr-2004

TrEMBL Release 26.2 of 26-Apr-2004

-
- Number of sequences found in Swiss-Prot₍₀₎ and TrEMBL₍₉₎: 9
 - Note that the selected sequences can be saved to a file to be later retrieved; to do so, go to the bottom of this page.
 - For more directed searches, you can use the Sequence Retrieval System SRS.
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Search in Swiss-Prot: There are matches to 0 out of 149913 entries

Search in TrEMBL: There are matches to 9 out of 1065889 entries

Sbjct: 244 KFLSAGPNATNLYYHLKRDYSLYLGYN YTF 273

tr Q9X750 **HopW protein precursor [HOPW] [Helicobacter pylori** 387
(**Campylobacter** AA
pylori]] align

Score = 136 bits (342), Expect = 4e-31
Identities = 102/335 (30%), Positives = 145/335 (42%), Gaps = 93/335 (27%)

Query: 21 EGDGVYIGTNYQLGQARLNSNIYNTGDC-----TGSVVGCPPGLTANK 63
E +G ++G + ++G+A +N Y G+ G GC P +
Sbjct: 61 EKNGAFVVGISLEVGRADQKTNAYRNGELFQVPFGDVSANDDGKVPNGQTGGCQPA-SGTP 119
Query: 64 HNPGGTN----INWHSKYA-----NGALNGFGLNVGYKKFFQFKSLDMSKWFGF 109
PG T +NW S+ N + G G+ GYK F K +WFG
Sbjct: 120 GTPGYTKANCVVNWTSRMTLSTNKNIPGRNQPMYGLGVMGTGYKHFIGKK-----RWFG 173
Query: 110 RVYGLFDYGHADLGKQVYAPNKI-----QLDMVSWGVGSDLLADIIDKDNASFGIFG 161
R YG FDYGH + A N I + DM ++G G+D+L +IIDK A+ G F
Sbjct: 174 RYYGFFDYGHNTNFSNS-RAANAISPFYLSQKADMYTYGFGTDMLFNIDKPKATAGFFV 232
Query: 162 GVAIGGNTWKSSAANYWKEQII-----EAKGPDVC---TPTYC---NPNAPY 202
GV GNTW ++ Y+K+ + A G C TP C NPN+ Y
Sbjct: 233 GVNFAAGTWTNNRVGYFKDGYVYGVNTDADAYMTNADGTITCGDTPASCDVGINPNSVY 292
Query: 203 ST-----NTSTVAFQVWLNFGVRANIYKHNGVEFGVRVPLLINKF-----L 243
+T + FQ +N G+R NI++H+G+EFG+++P L N F L
Sbjct: 293 TTGKLNKVNHTIFQFLVNVGIRTNIFEHHGIEFGIKIPTLPNYFFKGSTTIRAKKQG 352
Query: 244 SAGPNAT-----NLYYHLKRDYSLYLGYN YTF 270
G T +L L+R YS+YL Y YTF
Sbjct: 353 ENGQPTTITGAETNFSLTQTLRRQYSMYLRYVYTF 387

tr Q9ZJB9 **Putative outer membrane protein [JHP1394] [Helicobacter pylori** 388
J99 AA
(**Campylobacter pylori J99]]** align

Score = 135 bits (341), Expect = 5e-31
Identities = 102/335 (30%), Positives = 146/335 (43%), Gaps = 93/335 (27%)

Query: 21 EGDGVYIGTNYQLGQARLNSNIYNTGDC-----TGSVVGCPPGLTANK 63
E +G ++G + ++G+A +N Y G+ G GC P +
Sbjct: 62 EKNGAFVVGISLEVGRADQKTNAYRNGELFQVPFGDVSANDDGKVPDGTGGCQPA-SGTP 120
Query: 64 HNPGGTN----INWHSKYA-----NGALNGFGLNVGYKKFFQFKSLDMSKWFGF 109
PG T +NW S+ N + G G+ GYK F K +WFG
Sbjct: 121 GTPGYTKANCVVNWTSRMTLSTNKDIPGRNQPMYGLGVMGTGYKHFIGKK-----RWFG 174
Query: 110 RVYGLFDYGHADLGKQVYAPNKI-----QLDMVSWGVGSDLLADIIDKDNASFGIFG 161
R YG FDYGH + A N I + DM ++G G+D+L ++IDK A+ G F
Sbjct: 175 RYYGFFDYGHNTNFSNS-RAANAISPFYLSQKADMYTYGFGTDMLFNVIDKPKATAGFFV 233
Query: 162 GVAIGGNTWKSSAANYWKEQII-----EAKGPDVC---TPTYC---NPNAPY 202

```

          GV  GNTW ++  Y+K+  +          A G  C  TP  C  NPN+ Y
Sbjct: 234 GVNFAAGTWTNNRVGYFKDGYVYGVNTDADAYMTNADGTITCGDTPASCNVGINPNSVY 293

Query: 203 ST-----NTSTVAFQVWLNFGVRANIYKHNGVEFGVRVPLLINKFLSA-----GP- 247
          +T          +  FQ  +N G+R NI++H+G+EFG+++P L N F          GP
Sbjct: 294 TTGKLNKAVNHTIFQFLVNVGIRTNIFEHHGIEFGIKIPTLPNYFFKGSTTIRAKKQGPL 353

Query: 248 ---NAT-----NLYYHLKRDYSLYLGYNYTF 270
          N T          +L  L+R YS+YL Y YTF
Sbjct: 354 ENGNPTTITGAETNFSLTQTLRRQYSMYLRYVYTF 388

```

tr O26031 **Hypothetical protein HP1501 [HP1501] [Helicobacter pylori 388 AA (Campylobacter pylori)]**

align

Score = 135 bits (340), Expect = 7e-31
 Identities = 102/335 (30%), Positives = 145/335 (42%), Gaps = 93/335 (27%)

```

Query: 21  EGDGVYIGTNYQLGQARLNSNIYNTGDC-----TGSVVGCPPGLTANK 63
          E +G ++G + ++G+A  +N Y  G+          G  GC P  +
Sbjct: 62  EKNGAFVGVISLEVGRADQKTNAYKNGELFQVPFGDVSANDDGKVPDGTGGCQPA-SGTP 120

Query: 64  HNPGGTN----INWHSKYA-----NGALNGFGLNVGYKKFFQFKSLDMTSKWFGF 109
          PG T      +NW S+          N  + G G+  GYK F  K      +WFG
Sbjct: 121 GTPGYTKANCVVNWTSTRMLSTNKNIPGRNQPMYGLGVMTGYKHFIGKK-----RWFG 174

Query: 110 RVYGLFDYGHADLGKQVYAPNKI-----QLDMVSWGVGSDLLADIIDKDNASFGIFG 161
          R YG FDYGH +          A N I          + DM ++G G+D+L +IIDK A+ G F
Sbjct: 175 RYYGFFDYGHNTFNSNS-RAANAISPFYLSQKADMYTYGFGTDMLENIIDKPKATAGFFL 233

Query: 162 GVAIGNTWKSSAANYWKEQII-----EAKGPDVC---TPTYC---NPNAPY 202
          GV  GNTW ++  Y+K+  +          A G  C  TP  C  NPN+ Y
Sbjct: 234 GVNFAAGTWTNNRVGYFKDGYVYGVNTDADAYMTNADGTITCGDTPASCNVGINPNSVY 293

Query: 203 ST-----NTSTVAFQVWLNFGVRANIYKHNGVEFGVRVPLLINKF-----L 243
          +T          +  FQ  +N G+R NI++H+G+EFG+++P L N F          L
Sbjct: 294 TTGKLNKAVNHTIFQFLVNVGIRTNIFEHHGIEFGIKIPTLPNYFFKGSTTIRAKKQGPL 353

Query: 244 SAGPNAT-----NLYYHLKRDYSLYLGYNYTF 270
          G  T          +L  L+R YS+YL Y YTF
Sbjct: 354 ENGQPTTITGAETNFSLTQTLRRQYSMYLRYVYTF 388

```

tr O25382 **Outer membrane protein (OMP14) [HP0671] [Helicobacter pylori 270 AA (Campylobacter pylori)]**

align

Score = 115 bits (287), Expect = 9e-25
 Identities = 83/274 (30%), Positives = 125/274 (45%), Gaps = 72/274 (26%)

```

Query: 21  EGDGVYIGTNYQLGQARLNSNIYNTGDCTGSVVGCPPGLTANKHNPGGTNINWHSKYANG 80
          E +  Y+G +YQ+GQA  +          K+ P  +  N+  K+  G
Sbjct: 45  EKNAWYLGISYQVQASQSV-----KNPPKSSEFNY-PKFPVG 81

```

```

Query: 81  -----ALNGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLGK----- 124
          + G GL VGYK+FF K          +WFG R YG DYGHA G
Sbjct: 82  KTDYLAVMQGLGLTVGYKQFFGEK-----RWFGARYYGFM DYGHAVFGANALTS DNNGV 135

Query: 125 -QVYAPNKIQL-----DMVSWGVSDDLADIIDKDNASFGIFGGVAIGGNTWKSSAAN 176
          +++ P  ++          DM ++GVG D L ++I+K++ASFG F G I GN+W ++
Sbjct: 136 CELHQPCATKVGTMGNLSDMFTYGVGIDTLYNVINKEDASFGFFFGAQIAGNSWGNTTGA 195

Query: 177 YWKEQIIEAKGPDVCTPTYCNP NAPYSTNTSTVAFQVWLNFGVRANIYKHNGVEFGVRVP 236
          +   +E K P T   +P          FQ N G+R +I +H   +FGV++P
Sbjct: 196 F-----LETKSPYKHTSYSLDP-----AIFQFLFNLGIRTHIGRHQEFDFGVKIP 240

Query: 237 LLINKFLSAGPNATNLYYHLKRDYSLYLGYN YTF 270
          +   + + G   NL +   +R YSLY+GY Y F
Sbjct: 241 TINVYYFNHG----NLSFTYRRQYSLYVG YRYNF 270

```

tr Q9ZLG6 Putative outer membrane protein [JHP0614] [*Helicobacter pylori* 270
J99 AA
(*Campylobacter pylori* J99)] align

Score = 113 bits (283), Expect = 3e-24
Identities = 82/274 (29%), Positives = 121/274 (43%), Gaps = 72/274 (26%)

```

Query: 21  EGDGVYIGTNYQLGQARLNSNIYNTGDCTGSVVGCPPGLTANKHNPGGTNINWHSKYANG 80
          E + Y+G +YQ+GQA +          K+ P + N+ K+ G
Sbjct: 45  EKNAWYLGISYQVGQASQSV-----KNPPKSSEFNY-PKFPVG 81

Query: 81  -----ALNGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLGKQVYAPNKIQL 134
          + G GL VGYK+FF K          +WFG R YG DYGHA G   +   +
Sbjct: 82  KTDYLAVMQGLGLTVGYKQFFGEK-----RWFGARYYGFM DYGHAVFGANALTS DNNGV 135

Query: 135 -----DMVSWGVSDDLADIIDKDNASFGIFGGVAIGGNTWKSSAAN 176
          DM ++GVG D L ++I+K++ASFG F G I GN+W ++
Sbjct: 136 CKLNEPCATKVGTMGNLSDMFTYGVGIDTLYNVINKEDASFGFFFGAQIAGNSWGNTTGA 195

Query: 177 YWKEQIIEAKGPDVCTPTYCNP NAPYSTNTSTVAFQVWLNFGVRANIYKHNGVEFGVRVP 236
          +   +E K P T   +P          FQ N G+R +I +H   +FGV++P
Sbjct: 196 F-----LETKSPYKHTSYSLDP-----AIFQFLFNLGIRTHIGRHQEFDFGVKIP 240

Query: 237 LLINKFLSAGPNATNLYYHLKRDYSLYLGYN YTF 270
          +   + + G   NL +   +R YSLY+GY Y F
Sbjct: 241 TINVYYFNHG----NLSFTYRRQYSLYVG YRYNF 270

```

tr Q9ZMI3 Putative outer membrane protein [JHP0237] [*Helicobacter pylori* 479
J99 AA
(*Campylobacter pylori* J99)] align

Score = 98.2 bits (243), Expect = 1e-19
Identities = 63/207 (30%), Positives = 105/207 (50%), Gaps = 48/207 (23%)

```

Query: 77  YANGALNGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLGKQVYAPNKIQLDM 136
          Y + ++NGFG +GYK+FF K          K G R YG DYG+A+ G   K+ ++
Sbjct: 308 YQSASMNGFGAKMGYKQFFTHK-----KNIGLRYYGFLDYGYANFGD---TNLKVGANL 358

```

```
Query: 137 VSWGVGSDLLADIID----KDNASFGIFGGVAIGGNTWKSSAANYWKEQIIIEAKGPDVCT 192
      V++GVG+D L ++ +      ++ + G+F G I G TW ++ N      ++ + PDV
Sbjct: 359 VTYGVGTDFLYNVYERSRRRERTTIGLFFGAQIAGQTWSTNVTN-----LLSGQRPDV-- 411

Query: 193 PTYCNP NAPYSTNTSTVAFQVWLNFGVRANIYKHN-----GVEFGVRVPLLINK-FL 243
      + +FQ + GVR N K N      G+EFGV++P++ +K F
Sbjct: 412 -----KSSSFQFLFDLGVRTNFAKTNFNKHRLDQGIEFGVKIPVIAHKYFA 457

Query: 244 SAGPNATNLYYHLKRDYSLYLGYNYTF 270
      + G +A+ +      R++S Y+GY+ F
Sbjct: 458 TQGSSASYM-----RNFSFYVGYSVGF 479
```

tr Q9X752 **HopZ protein precursor [HOPZ] [Helicobacter pylori** 485
 (Campylobacter AA
 pylori)] align

Score = 98.2 bits (243), Expect = 1e-19
Identities = 63/207 (30%), Positives = 105/207 (50%), Gaps = 48/207 (23%)

```
Query: 77 YANGALNGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLGKQVYAPNKIQLDM 136
      Y + ++NGFG +GYK+FF K      K G R YG DYG+A+ G      K+ ++
Sbjct: 314 YQSASMNGFGAKMGYKQFFTHK-----KNIGLRYYGFLDYGYANFGD---TNLKVGANL 364

Query: 137 VSWGVGSDLLADIID----KDNASFGIFGGVAIGGNTWKSSAANYWKEQIIIEAKGPDVCT 192
      V++GVG+D L ++ +      ++ + G+F G I G TW ++ N      ++ + PDV
Sbjct: 365 VTYGVGTDFLYNVYERSRRRERTTIGLFFGAQIAGQTWSTNVTN-----LLSGQRPDV-- 417

Query: 193 PTYCNP NAPYSTNTSTVAFQVWLNFGVRANIYKHN-----GVEFGVRVPLLINK-FL 243
      + +FQ + GVR N K N      G+EFGV++P++ +K F
Sbjct: 418 -----KSSSFQFLFDLGVRTNFAKTNFNKHRLDQGIEFGVKIPVIAHKYFA 463

Query: 244 SAGPNATNLYYHLKRDYSLYLGYNYTF 270
      + G +A+ +      R++S Y+GY+ F
Sbjct: 464 TQGSSASYM-----RNFSFYVGYSVGF 485
```

tr O25034 **Outer membrane protein (OMP7) [HP0252] [Helicobacter pylori** 487 AA
 (Campylobacter pylori)] align

Score = 97.8 bits (242), Expect = 2e-19
Identities = 63/207 (30%), Positives = 105/207 (50%), Gaps = 48/207 (23%)

```
Query: 77 YANGALNGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLGKQVYAPNKIQLDM 136
      Y + ++NGFG +GYK+FF K      K G R YG DYG+A+ G      K+ ++
Sbjct: 316 YQSASMNGFGAKMGYKQFFTHK-----KNVGLRYYGFLDYGYANFGD---TNLKVGANL 366

Query: 137 VSWGVGSDLLADIID----KDNASFGIFGGVAIGGNTWKSSAANYWKEQIIIEAKGPDVCT 192
      V++GVG+D L ++ +      ++ + G+F G I G TW ++ N      ++ + PDV
Sbjct: 367 VTYGVGTDFLYNVYERSRRRERTTIGLFFGAQIAGQTWSTNVTN-----LLSGQRPDV-- 419

Query: 193 PTYCNP NAPYSTNTSTVAFQVWLNFGVRANIYKHN-----GVEFGVRVPLLINK-FL 243
      + +FQ + GVR N K N      G+EFGV++P++ +K F
```

Sbjct: 420 -----KSSSFQFLFDLGVRTNFAKTNFNKHRLDQGIEFGVKIPVIAHKYFA 465
Query: 244 SAGPNATNLYYHLKRDYSLYLGYN YTF 270
+ G +A+ + R++S Y+GY+ F
Sbjct: 466 TQGSSASYM-----RNFSFYVGYSVGF 487

tr Q8GDJ2 HopQ [HOPQ] [Helicobacter pylori (Campylobacter
pylori)] 631 AA
align

Score = 97.8 bits (242), Expect = 2e-19
Identities = 75/226 (33%), Positives = 107/226 (47%), Gaps = 49/226 (21%)

Query: 64 HNPGGTNINWHSKYANGALNGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLG 123
HNP S+ NGA+NG G+ VGYK+FF K K +G R YG FDY HA +
Sbjct: 436 HNPFKRVGIISSQTNNGAMNGLGVQVGYKQFFGEK-----KRWGLRYYGFFDYNHAYIK 489
Query: 124 KQVYAPNKIQLDMVSWGVGSDLLADIIDKDNA-----SFGIFGGVAIGGNTWKSSA 174
+ D+ ++GVGSDLL + I+ N SFG+FGG+A+ G +W +S
Sbjct: 490 SNFF---NSASDVWTYGVGSDLLFNFINDKNTNFLGKNNQISFGLFGGIALAGTSWLNS- 545
Query: 175 ANYWKEQIIIEAKGPDVCTPTYCNPAPYSTNTSTVAFQVWLNFGVRANIYK----- 225
Q + K T N YS +T FQ N G+R N+ +
Sbjct: 546 -----QFVNLK-----TISN---VYSAKVNTANFQFLFNLGLRTNLARPKKKDSHHA 589
Query: 226 -HNGVEFGVRVPLLINKFLSAGPNATNLYYHLKRDYSLYLGYN YTF 270
+G+E GV++P + + S T L Y +R YS+YL Y + +
Sbjct: 590 AQHGMELGVKIPTINTNYYSF--LDTKLEY--RRLYSVYLN YVFAY 631

tr Q8GDJ3 HopQ [HOPQ] [Helicobacter pylori (Campylobacter
pylori)] 630 AA
align

Score = 97.8 bits (242), Expect = 2e-19
Identities = 75/226 (33%), Positives = 107/226 (47%), Gaps = 49/226 (21%)

Query: 64 HNPGGTNINWHSKYANGALNGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLG 123
HNP S+ NGA+NG G+ VGYK+FF K K +G R YG FDY HA +
Sbjct: 435 HNPFKRVGIISSQTNNGAMNGLGVQVGYKQFFGEK-----KRWGLRYYGFFDYNHAYIK 488
Query: 124 KQVYAPNKIQLDMVSWGVGSDLLADIIDKDNA-----SFGIFGGVAIGGNTWKSSA 174
+ D+ ++GVGSDLL + I+ N SFG+FGG+A+ G +W +S
Sbjct: 489 SNFF---NSASDVWTYGVGSDLLFNFINDKNTNFLGKNNQISFGLFGGIALAGTSWLNS- 544
Query: 175 ANYWKEQIIIEAKGPDVCTPTYCNPAPYSTNTSTVAFQVWLNFGVRANIYK----- 225
Q + K T N YS +T FQ N G+R N+ +
Sbjct: 545 -----QFVNLK-----TISN---VYSAKVNTANFQFLFNLGLRTNLARPKKKDSHHG 588
Query: 226 -HNGVEFGVRVPLLINKFLSAGPNATNLYYHLKRDYSLYLGYN YTF 270
+G+E GV++P + + S T L Y +R YS+YL Y + +
Sbjct: 589 AQHGMELGVKIPTINTNYYSF--LDTKLEY--RRLYSVYLN YVFAY 630

tr Q9X745 HopZ protein precursor [HOPZ] [Helicobacter pylori] 668
(Campylobacter
pylori)] AA
align

Score = 97.1 bits (240), Expect = 3e-19
Identities = 73/222 (32%), Positives = 106/222 (46%), Gaps = 45/222 (20%)

Query: 64 HNPGGTNINWHSKYANGALNGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLG 123
HNP S+ NGA+NG G+ VGYK+FF K KW G R YG FDY HA +
Sbjct: 477 HNPFRRVGLISSQTNGAMNGIGVQVGYKQFFGEK-----RKW-GLRYYGFFDYNHAYIK 530

Query: 124 KQVYAPNKKIQLDMVSWGVGSDLLADIID-----KDNASFGIFGGVAIGGNTWKSSAANYW 178
+ D+ ++GVG+D+L + I+ + SFG+FGG+A+ G +W +S
Sbjct: 531 SSFF---NSASDVFTYGVGTDVLYNFINDKATKNNKISFGVFGGIALAGTSWLNSQY--- 584

Query: 179 KEQIIIEAKGPDVCTPTYCNPAPYSTNTSTVAFQVWLNFGVRANIYKH-----NG 228
V T+ N YS + FQ N G+R N+ K+ +G
Sbjct: 585 -----VNLATF---NNFYSAKMNVANFQFLFNLGLRMNLAKNKKKASDHAAQHG 630

Query: 229 VEFGRVPLLINKFLSAGPNATNLYYHLKRDYSLYLGYN YTF 270
VE GV++P + + S T L Y +R YS+YL Y + +
Sbjct: 631 VELGVKIPTINTNYYSL--LGTQLQY--RRLYSVYLN YVFAY 668

tr O25015 Outer membrane protein (OMP6) [HP0229] [Helicobacter pylori] 483 AA
(Campylobacter pylori)]
align

Score = 96.7 bits (239), Expect = 3e-19
Identities = 71/208 (34%), Positives = 102/208 (48%), Gaps = 36/208 (17%)

Query: 64 HNPGGTNINWHSKYANGALNGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLG 123
HNP + +S+ NGA+NG G+ +GYK+FF +K+FG R Y FDY HA +
Sbjct: 303 HNPFRSVGLINSQSNNGAMNGVGVQLGYKQFFG-----KNKFFGIRYYAFFDYNHAYIK 356

Query: 124 KQVYAPNKKIQLDMVSWGVGSDLLADIID-----DKDN-ASFGIFGGVAIGGNTWKSSAANYW 178
+ ++ ++G GSDLL + I DK+ SFGIFGG+A+ G TW +S
Sbjct: 357 SNFFNSAS---NVFTYAGSDLLLNFINNGSDKNRKVSFGIFGGIALAGTTWLNS----- 408

Query: 179 KEQIIIEAKGPDVCTPTYCNPAPYSTNTSTVAFQVWLNFGVRANIYKHNGVEFGVRVPLL 238
Q + K N+ YS + FQ N G+R H+GVE GV++P +
Sbjct: 409 --QFMNLK-----TTNSAYSAKINNTNFQFLFNTGLRLQGI-HHGVELGVKIPTI 455

Query: 239 INKFLSAGPNATNLYYHLKRDYSLYLG Y 266
+ S L Y +R YS+Y Y
Sbjct: 456 NTNYYSF--MGAKLAY--RRLYSVYFNY 479

tr Q8GDI8 HopQ [HOPQ] [Helicobacter pylori (Campylobacter pylori)] 632 AA
align

Score = 96.7 bits (239), Expect = 3e-19
Identities = 74/226 (32%), Positives = 107/226 (46%), Gaps = 49/226 (21%)

Query: 64 HNPGGTNINWHSKYANGALNGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLG 123

```

      HNP      S+   NGA+NG G+ VGYK+FF  K      K +G R YG FDY HA +
Sbjct: 437 HNPFKRVGIISSQTNNNGAMNGLGVQVGYKQFFGEK-----KRWGLRYYGFFDYNHAYIK 490

Query: 124 KQVYAPNKIQLDMSVSWGVGSDLLADIIDKDNASF-----GIFGGVAIGGNTWKSSA 174
      +      D+ ++GVGSDLL + I+  N +F      G+FGG+A+ G +W +S
Sbjct: 491 SNFF--NSASDVWTYGVGSDLLFNFINDKNTNFLGKNNQISVGLFGGIALAGTSWLNS- 546

Query: 175 ANYWKEQIIEAKGPDVCTPTYCNPAPYSTNTSTVAFQVWLNFGVRANIYK----- 225
      Q + K      T N      YS +T FQ  N G+R N+ +
Sbjct: 547 -----QFVNLK-----TISN---VYSAKVNTANFQFLFNLGLRTNLRPKKKDSHHA 590

Query: 226 -HNGVEFGVRVPLLINKFLSAGPNATNLYYHLKRDYSLYLGYN YTF 270
      +G+E GV++P +      + S      T L Y +R YS+YL Y + +
Sbjct: 591 GQHGMELGVKIPTINTNYYSF--LDTKLEY--RRLYSVYLN YVFAY 632

```

tr Q8GDJ1 **HopQ [HOPQ] [Helicobacter pylori (Campylobacter pylori)]** 629 AA align

Score = 96.7 bits (239), Expect = 3e-19

Identities = 74/226 (32%), Positives = 107/226 (46%), Gaps = 49/226 (21%)

```

Query: 64 HNPGGTNINWHISKYANGALNGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLG 123
      HNP      S+   NGA+NG G+ VGYK+FF  K      K +G R YG FDY HA +
Sbjct: 434 HNPFKRVGIISSQTNNNGAMNGLGVQVGYKQFFGEK-----KRWGLRYYGFFDYNHAYIK 487

Query: 124 KQVYAPNKIQLDMSVSWGVGSDLLADIIDKDNASF-----GIFGGVAIGGNTWKSSA 174
      +      D+ ++GVGSDLL + I+  N +F      G+FGG+A+ G +W +S
Sbjct: 488 SSFF--NSASDVWTYGVGSDLLFNFINDKNTNFLGKNNQISVGLFGGIALAGTSWLNS- 543

Query: 175 ANYWKEQIIEAKGPDVCTPTYCNPAPYSTNTSTVAFQVWLNFGVRANIYK----- 225
      Q + K      T N      YS +T FQ  N G+R N+ +
Sbjct: 544 -----QFVNLK-----TISN---VYSAKVNTANFQFLFNLGLRTNLRPKKKDSHHA 587

Query: 226 -HNGVEFGVRVPLLINKFLSAGPNATNLYYHLKRDYSLYLGYN YTF 270
      +G+E GV++P +      + S      T L Y +R YS+YL Y + +
Sbjct: 588 GQHGMELGVKIPTINTNYYSF--LDTKLEY--RRLYSVYLN YVFAY 629

```

tr Q8GDJ4 **HopQ [HOPQ] [Helicobacter pylori (Campylobacter pylori)]** 634 AA align

Score = 96.7 bits (239), Expect = 3e-19

Identities = 71/211 (33%), Positives = 102/211 (47%), Gaps = 49/211 (23%)

```

Query: 79 NGALNGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLGKQVYAPNKIQLDMSV 138
      NGALNG G+ VGYK+FF  K      K +G R YG FDY HA +      +      D+ +
Sbjct: 454 NGALNGLGVQVGYKQFFGEK-----KRWGLRYYGFFDYNHAYIKSNFF--NSASDVWT 504

Query: 139 WGVGSDLLADIIDKDNASF-----GIFGGVAIGGNTWKSSAANYWKEQIIEAKGPD 189
      +GVGSDLL + I+  N +F      G+FGG+A+ G +W +S      Q + K
Sbjct: 505 YGVGSDLLFNFINDKNTNFLGKNNQISVGLFGGIALAGTSWLNS-----QFVNLK--- 554

Query: 190 VCTPTYCNPAPYSTNTSTVAFQVWLNFGVRANIYK-----HNGVEFGVRVPLLI 239
      T N      YS +T FQ  N G+R N+ +      +G+E GV++P +

```

Sbjct: 555 ----TISN---VYSAKVNTANFQFLFNGLRNLARPKKKDSHAAQHGMELGVKIPTIN 607

Query: 240 NKFLSAGPNATNLYYHLKRDYSLYLGYNITF 270

+ S T L Y +R YS+YL Y + +

Sbjct: 608 TNYYSF--LDTKLEY--RRLYSVYLNIVFAY 634

tr Q9ZK39 Putative outer membrane function [JHP1103] [Helicobacter pylori J99] 643 AA
(Campylobacter pylori J99)] align

Score = 95.9 bits (237), Expect = 6e-19

Identities = 69/215 (32%), Positives = 104/215 (48%), Gaps = 49/215 (22%)

Query: 75 SKYANGALNGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLGKQVYAPNKIQL 134
S+ NGA+NG G+ GYK+FF K +W G R YG FDY H + + +

Sbjct: 459 SQTNGAMNGLGVQAGYKQFFGQK-----RRW-GLRYYGFFDYNHTYIKSSFFNSSS--- 509

Query: 135 DMVSWGVSDDLADIIDKDNASF-----GIFGGVAIGGNTWKSSAANYWKEQIIEA 185
D++++GVGSDLL + I+ N +F G+FGG+A+ G +W +S Q +

Sbjct: 510 DVLTYGVGSDLLFNFINDKNTNFLGKNNKISVGLFGGIALAGTSWLNS-----QFVNL 562

Query: 186 KGPDVCTPTYCNPAPYSTNTSTVAFQVWLNFGVRANIYK-----HNGVEFGVRV 235
K T N YS +T FQ N G+R N+ + +G+E GV++

Sbjct: 563 K-----TISN---VYSAKVNTANFQFLFNGLRNLARPKKKDSHAAQHGMELGVKI 612

Query: 236 PLLINKFLSAGPNATNLYYHLKRDYSLYLGYNITF 270

P + + S T L Y +R YS+YL Y + +

Sbjct: 613 PTINTNYYSY--LGTKLEY--RRLYSVYLNIVFAY 643

tr Q9ZMK5 Outer membrane protein/porin [HOPA] [Helicobacter pylori J99] 483 AA
(Campylobacter pylori J99)] align

Score = 95.9 bits (237), Expect = 6e-19

Identities = 68/208 (32%), Positives = 101/208 (47%), Gaps = 36/208 (17%)

Query: 64 HNPGGTNINWHISKYANGALNGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLG 123
HNP + +S+ NGA+NG G+ +GYK+FF +K+FG R YG FDY +A +

Sbjct: 303 HNPFRSVGLINSQSNNGAMNGVGVQLGYKQFFG-----KNKFFGIRYYGFFDYNAYIK 356

Query: 124 KQVYAPNKIQLDMVSWGVSDDLADIID-----KDNASFGIFGGVAIGGNTWKSSAANYW 178
+ ++ ++G GSDLL + I+ SFGIFGG+A+ G TW ++ +

Sbjct: 357 SNFF--NSASNVFTYGAGSDLLNFINGGSDRNRKVSFGIFGGIALAGTTWLNNQSANL 413

Query: 179 KEQIIEAKGPDVCTPTYCNPAPYSTNTSTVAFQVWLNFGVRANIYKHNGVEFGVRVPLL 238
K N+ YS + FQ N G+R H+G+E GV++P +

Sbjct: 414 K-----ITNSAYSAKINNTNFQFLFNTGLRLQGI-HHGIELGVKIPTI 455

Query: 239 INKFLSAGPNATNLYYHLKRDYSLYLGYNITF 266

+ S L Y +R YSLYL Y

Sbjct: 456 NTNYYSF--MGAKLAY--RRLYSVYLNIVFAY 479

tr Q8GDJ0 **HopQ [HOPQ] [Helicobacter pylori (Campylobacter pylori)]** 640 AA
align

Score = 95.9 bits (237), Expect = 6e-19

Identities = 73/226 (32%), Positives = 106/226 (46%), Gaps = 49/226 (21%)

Query: 64 HNPGGTNINWHSKYANGALNGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLG 123
HNP S+ NGA+NG G+ GYK+FF K K +G R YG FDY HA +
Sbjct: 445 HNPFKRVGIISSQTNNGAMNGLGVQAGYKQFFGEK-----KRWGLRYYGFFDYNHAYIK 498

Query: 124 KQVYAPNKIQLDMVSWGVSDDLADIIDKDNASF-----GIFGGVAIGGNTWKSSA 174
+ D+ ++GVGSDLL + I+ N +F G+FGG+A+ G +W +S
Sbjct: 499 SNFF---NSASDVWTYGVGSDLLFNFINDKNTNFLGKNNKISVGLFGGIALAGTSLWNS- 554

Query: 175 ANYWKEQIIEAKGPDVCTPTYCNPAPYSTNTSTVAFQVWLNFGVRANIYK----- 225
Q + K T N YS +T FQ N G+R N+ +
Sbjct: 555 -----QFVNLK-----TISN---VYSAKVNTANFQFLFNLGLRTNLRPKKKDSHHA 598

Query: 226 -HNGVEFGVRVPLLINKFLSAGPNATNLYYHLKRDYSLYLGYN YTF 270
+G+E GV++P + + S T L Y +R YS+YL Y + +
Sbjct: 599 AQHGMELGVKIPTITTNYYSF--LDTKLEY--RRLYSVYLN YVFAY 640

tr Q9X747 **HopZ protein precursor [HOPZ] [Helicobacter pylori (Campylobacter pylori)]** 669
AA
align

Score = 95.9 bits (237), Expect = 6e-19

Identities = 72/222 (32%), Positives = 106/222 (47%), Gaps = 45/222 (20%)

Query: 64 HNPGGTNINWHSKYANGALNGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLG 123
HNP S+ NGA+NG G+ VGYK+FF K +W G R YG FDY HA +
Sbjct: 478 HNPFRRVGLISSQTNNGAMNGIGVQVG YKQFFGEK-----RRW-GLRYYGFFDYNHAYIK 531

Query: 124 KQVYAPNKIQLDMVSWGVSDDLADIID-----KDNASFGIFGGVAIGGNTWKSSAANYW 178
+ D+ ++GVG+D+L + I+ + SFG+FGG+A+ G +W +S
Sbjct: 532 SSFF---NSASDVFTYGVGTDVLYNFINDKATKNNKISFGVFGGIALAGTSLWNSQY--- 585

Query: 179 KEQIIEAKGPDVCTPTYCNPAPYSTNTSTVAFQVWLNFGVRANIYKH-----NG 228
V T+ N YS + FQ N G+R N+ K+ +G
Sbjct: 586 -----VNLATF---NNFYSAKMNVANFQFLFNLGLRMNLAKNKKKASDHVAQHG 631

Query: 229 VEFQVVRVPLLINKFLSAGPNATNLYYHLKRDYSLYLGYN YTF 270
VE GV++P + + S T L Y +R YS+YL Y + +
Sbjct: 632 VELGVKIPTINTNYYSL--LGTQLQY--RRLYSVYLN YVFAY 669

tr Q9ZN51 **Putative outer membrane protein [JHP0007] [Helicobacter pylori J99 (Campylobacter pylori J99)]** 668
AA
align

Score = 95.5 bits (236), Expect = 8e-19

Identities = 72/222 (32%), Positives = 105/222 (46%), Gaps = 45/222 (20%)

Query: 64 HNPGGTNINWHSKYANGALNGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLG 123
HNP S+ NGA+NG G+ VGYK+FF K +W G R YG FDY HA +
Sbjct: 477 HNPFRRVGLISSQTNGAMNGIGVQVGYKQFFGEK-----RRW-GLRYYGFFDYNHAYIK 530

Query: 124 KQVYAPNKIQLDMSVSWGVGSDLLADIID-----KDNASFGIFGGVAIGGNTWKSSAANYW 178
+ D+ ++GVG+D+L + I+ SFG+FGG+A+ G +W +S
Sbjct: 531 SSFF---NSASDVFTYGVGTDVLYNFINDKTTKNSKISFGVFGGIALAGTSWLNSQY--- 584

Query: 179 KEQIEAKGPDVCTPTYCNPAPYSTNTSTVAFQVWLNFGVRANIYKH-----NG 228
V T+ N YS + FQ N G+R N+ K+ +G
Sbjct: 585 -----VNLATF---NNFYSAKMNVANFQFLFNLGLRMNLAKNKKKASDHAAQHG 630

Query: 229 VEFQVVRVPLLINKFLSAGPNATNLYYHLKRDYSLYLGYNITF 270
VE GV++P + + S T L Y +R YS+YL Y + +
Sbjct: 631 VELGVKIPTINTNYISL--LGTQLQY--RRLYSVYLNIVFAY 668

tr Q9X746 HopZ protein precursor [HOPZ] [Helicobacter pylori] 699
(Campylobacter AA
pylori)] align

Score = 95.5 bits (236), Expect = 8e-19
Identities = 72/222 (32%), Positives = 106/222 (47%), Gaps = 45/222 (20%)

Query: 64 HNPGGTNINWHSKYANGALNGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLG 123
HNP S+ NGA+NG G+ +GYK+FF K KW G R YG FDY HA +
Sbjct: 508 HNPFRRVGLISSQTNGAMNGIGVQIGYKQFFGEK-----RKW-GARYYGFFDYNHAYIK 561

Query: 124 KQVYAPNKIQLDMSVSWGVGSDLLADIID-----KDNASFGIFGGVAIGGNTWKSSAANYW 178
+ D+ ++GVG+D+L + I+ + SFG+FGG+A+ G +W +S
Sbjct: 562 SSFF---NSASDVFTYGVGTDVLYNFINDKATKNNKISFGVFGGIALAGTSWLNSQY--- 615

Query: 179 KEQIEAKGPDVCTPTYCNPAPYSTNTSTVAFQVWLNFGVRANIYKH-----NG 228
V T+ N YS + FQ N G+R N+ K+ +G
Sbjct: 616 -----VNLATF---NNFYSAKMNVANFQFLFNLGLRMNLAKNKKKASDHAAQHG 661

Query: 229 VEFQVVRVPLLINKFLSAGPNATNLYYHLKRDYSLYLGYNITF 270
VE GV++P + + S T L Y +R YS+YL Y + +
Sbjct: 662 VELGVKIPTINTNYISL--LGTQLEY--RRLYSVYLNIVFAY 699

tr Q9X748 HopZ protein precursor [HOPZ] [Helicobacter pylori] 667
(Campylobacter AA
pylori)] align

Score = 95.5 bits (236), Expect = 8e-19
Identities = 72/222 (32%), Positives = 106/222 (47%), Gaps = 45/222 (20%)

Query: 64 HNPGGTNINWHSKYANGALNGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLG 123
HNP S+ NGA+NG G+ VGYK+FF K +W G R YG FDY HA +
Sbjct: 476 HNPFRRVGLISSQTNGAMNGIGVQVGYKQFFGEK-----RRW-GLRYYGFFDYNHAYIK 529

Query: 124 KQVYAPNKIQLDMSVSWGVGSDLLADIID-----KDNASFGIFGGVAIGGNTWKSSAANYW 178
+ D+ ++GVG+D+L + I+ + SFG+FGG+A+ G +W +S
Sbjct: 530 SSFF---NSASDVFTYGVGTDVLYNFINDKATKNNKISFGVFGGIALAGTSWLNSQY--- 583

```
Query: 179 KEQIIIEAKGPDVCTPTYCNPAPYSTNTSTVAFQVWLNFGVRANIYKH-----NG 228
          V  T+  N  YS  +  FQ  N G+R N+ K+          +G
Sbjct: 584 -----VNLATF---NNFYSAKMNVANFQFLFNLGLRMNLAKNKKKASDHVAQHG 629

Query: 229 VEFQVVRVPLLINKFLSAGPNATNLYYHLKRDYSLYLGYNITF 270
          VE GV++P +   + S      T L Y  +R YS+YL Y + +
Sbjct: 630 VELGVKIPTINTNYISL--LGTQLEY--RRLYSVYLNIVVFAY 667
```

tr Q8GDI6 **HopQ [HOPQ] [Helicobacter pylori (Campylobacter pylori)]** 632 AA
align

Score = 95.1 bits (235), Expect = 1e-18
Identities = 73/226 (32%), Positives = 106/226 (46%), Gaps = 49/226 (21%)

```
Query: 64  HNPGGTNINWHSKYANGALNGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLG 123
          HNP      S+  NGA+NG G+ VGYK+FF  K      K +G R YG FDY H  +
Sbjct: 437 HNPFKRVGIISSQTNNGAMNGLGVQVGYKQFFGEK-----KRWGLRYYGFFDYNHTYIK 490

Query: 124 KQVYAPNKKIQLDMVSWGVGSDLLADIIDKDNASF-----GIFGGVAIGGNTWKSSA 174
          +      D+ ++GVGSDLL + I+  N +F      G+FGG+A+ G +W +S
Sbjct: 491 SNFF---NSASDVWTYGVGSDLLFNFINDKNTNFLGKNNQISVGLFGGIALAGTSLWLS- 546

Query: 175 ANYWKEQIIIEAKGPDVCTPTYCNPAPYSTNTSTVAFQVWLNFGVRANIYK----- 225
          Q + K      T  N      YS  +T  FQ  N G+R N+ +
Sbjct: 547 -----QFVNLK-----TISN---VYSAKVNTANFQFLFNLGLRTNLARPKKKDSHHA 590

Query: 226 -HNGVEFGVVRVPLLINKFLSAGPNATNLYYHLKRDYSLYLGYNITF 270
          +G+E GV++P +   + S      T L Y  +R YS+YL Y + +
Sbjct: 591 GQHGMEELGVKIPTINTNYISF--LDTKLEY--RRLYSVYLNIVVFAY 632
```

tr Q8GDI7 **HopQ [HOPQ] [Helicobacter pylori (Campylobacter pylori)]** 632 AA
align

Score = 95.1 bits (235), Expect = 1e-18
Identities = 73/226 (32%), Positives = 106/226 (46%), Gaps = 49/226 (21%)

```
Query: 64  HNPGGTNINWHSKYANGALNGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLG 123
          HNP      S+  NGA+NG G+ VGYK+FF  K      K +G R YG FDY H  +
Sbjct: 437 HNPFKRVGIISSQTNNGAMNGLGVQVGYKQFFGEK-----KRWGLRYYGFFDYNHTYIK 490

Query: 124 KQVYAPNKKIQLDMVSWGVGSDLLADIIDKDNASF-----GIFGGVAIGGNTWKSSA 174
          +      D+ ++GVGSDLL + I+  N +F      G+FGG+A+ G +W +S
Sbjct: 491 SNFF---NSASDVWTYGVGSDLLFNFINDKNTNFLGKNNQISVGLFGGIALAGTSLWLS- 546

Query: 175 ANYWKEQIIIEAKGPDVCTPTYCNPAPYSTNTSTVAFQVWLNFGVRANIYK----- 225
          Q + K      T  N      YS  +T  FQ  N G+R N+ +
Sbjct: 547 -----QFVNLK-----TISN---VYSAKVNTANFQFLFNLGLRTNLARPKKKDSHHA 590

Query: 226 -HNGVEFGVVRVPLLINKFLSAGPNATNLYYHLKRDYSLYLGYNITF 270
          +G+E GV++P +   + S      T L Y  +R YS+YL Y + +
Sbjct: 591 GQHGMEELGVKIPTINTNYISF--LDTKLEY--RRLYSVYLNIVVFAY 632
```

tr Q9ZMV0 Putative outer membrane protein [JHP0117] [*Helicobacter pylori* 286
J99 AA
(*Campylobacter pylori* J99)] align

Score = 94.7 bits (234), Expect = 1e-18

Identities = 79/274 (28%), Positives = 116/274 (41%), Gaps = 49/274 (17%)

```

Query: 21  EGDGVYIGTNYQLGQARLNSNIYNTGDCTGSVVGCPPGLTANK---HNP-----GGTNI 71
           E +  +IG +YQLG      +  + G+C G+  G      T N      NP      G
Sbjct: 38  ERNAAFIGIDYQLGMLSTTAQNCSHGNCNGNQSGAYGSNTPNMPTASNPTGGLTHGALGT 97

Query: 72  NWHISKYANG--ALNGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLGKQVY-- 127
           +  +N  A+NGFG  VGYK FF+      +  FG R YG FD+  +      Y
Sbjct: 98  RGYKGLSNQQYAINGFGFVVGYKHFFK-----KAPQFGMRYYGFFDFASSYYKYTYND 151

Query: 128  -----APNKIQLDMVSWGVGSDLLAD--IIDKDNASFGIFGGVAIGGNTWKSSAANYWKE 180
           A   Q  M  +G G+D+L +  I +++N  FG F GVAIGG +W      NY+  +
Sbjct: 152  YGMRDARKGSQSFMFYAGAGTDVLFNPAIFNRENLFHFGFFLGVAIGGTSW--GPTNYYFK 209

Query: 181  QIIEAKGPDVCTPTYCNPAPYSTNTSTVAFQVWLNFGVRANIYKHNGVEFGVRVPLLIN 240
           + E                               Y  +      FQV +N G+R      KH G E G+++  + N
Sbjct: 210  DLAE-----EYRGSFHPSNFQVLVNGGIRLGT-KHQGF EIGLKIQTIRN 252

Query: 241  KFLSAG----PNATNLYYHLKRDYSLYLGYN YTF 270
           + +A      P  T  +  R Y+ Y  Y  +F
Sbjct: 253  NYYTASADNVPEGTTYRFTFHRPYAFYWRYIVSF 286

```

tr O24941 Hypothetical protein HP0127 [HP0127] [*Helicobacter pylori* 286 AA
(*Campylobacter pylori*)] align

Score = 94.7 bits (234), Expect = 1e-18

Identities = 79/274 (28%), Positives = 116/274 (41%), Gaps = 49/274 (17%)

```

Query: 21  EGDGVYIGTNYQLGQARLNSNIYNTGDCTGSVVGCPPGLTANK---HNP-----GGTNI 71
           E +  +IG +YQLG      +  + G+C G+  G      T N      NP      G
Sbjct: 38  ERNAAFIGIDYQLGMLSTTAQNCSHGNCNGNQSGAYGSNTPNMPTASNPTGGFTHGALGT 97

Query: 72  NWHISKYANG--ALNGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLGKQVY-- 127
           +  +N  A+NGFG  VGYK FF+      S  FG R YG FD+  +      Y
Sbjct: 98  RGYKGLSNQQYAINGFGFVVGYKHFFK-----KSPQFGMRYYGFFDFASSYYKYTYND 151

Query: 128  -----APNKIQLDMVSWGVGSDLLAD--IIDKDNASFGIFGGVAIGGNTWKSSAANYWKE 180
           A   Q  M  +G G+D+L +  I +++N  FG F GVAIGG +W      NY+  +
Sbjct: 152  YGMRDARKGSQSFMFYAGAGTDVLFNPAIFNRENLFHFGFFLGVAIGGTSW--GPTNYYFK 209

Query: 181  QIIEAKGPDVCTPTYCNPAPYSTNTSTVAFQVWLNFGVRANIYKHNGVEFGVRVPLLIN 240
           + +                               Y  +      FQV +N G+R      KH G E G+++  + N
Sbjct: 210  DLAD-----EYRGSFHPSNFQVLVNGGIRLGT-KHQGF EIGLKIQTIRN 252

Query: 241  KFLSAG----PNATNLYYHLKRDYSLYLGYN YTF 270
           + +A      P  T  +  R Y+ Y  Y  +F
Sbjct: 253  NYYTASADNVPEGTTYRFTFHRPYAFYWRYIVSF 286

```

tr Q9ZKS8 Putative outer membrane protein [JHP0857] [Helicobacter pylori 366
J99 AA
(Campylobacter pylori J99)] align

Score = 93.6 bits (231), Expect = 3e-18
Identities = 62/196 (31%), Positives = 92/196 (46%), Gaps = 25/196 (12%)

Query: 81 ALNGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLGKQVYAPNKI----QLDM 136
++ G GL+VGYK FF K K GFR Y +DYG+ + G + N +++
Sbjct: 190 SMYGVGLSVGYKHFFTKK-----KNQGFYYLFYDYGYNFNG---FVGNFGDGLGKMNN 240

Query: 137 VSWGVGSDLLADIID--KDNASFGIFGGVAIGGNTWKSSAANYWKEQIIIEAKGPDVCTPT 194
+G+G D L + ID + ++S G + G A+ G++W S W Q+
Sbjct: 241 HLYGLGIDYLFNFIDNAQKHSSVGFYVGFALAGSSWVGSGGLGMWVSQMDFIN----- 292

Query: 195 YCNP NAPYSTNTSTVAFQVWLNFGVRANIYKHNGVEFGVRVPLLINKFLSAGPNATNLYY 254
N Y T FQ+ LNFGVR N+ +HNG E G+++PL +N F N
Sbjct: 293 --NYLTDYRAKMHTSFFQIPLNFGVRVNVDRHNGFEMGLKIPLAVNSFYETHGKGLNASL 350

Query: 255 HLKRDYSLYLGYN YTF 270
KR + Y Y+F
Sbjct: 351 FFKRLVMFNVS YVYSF 366

tr Q9ZLZ6 Putative outer membrane protein [JHP0429] [Helicobacter pylori 371
J99 AA
(Campylobacter pylori J99)] align

Score = 93.6 bits (231), Expect = 3e-18
Identities = 62/196 (31%), Positives = 92/196 (46%), Gaps = 25/196 (12%)

Query: 81 ALNGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLGKQVYAPNKI----QLDM 136
++ G GL+VGYK FF K K GFR Y +DYG+ + G + N +++
Sbjct: 195 SMYGVGLSVGYKHFFTKK-----KNQGFYYLFYDYGYNFNG---FVGNFGDGLGKMNN 245

Query: 137 VSWGVGSDLLADIID--KDNASFGIFGGVAIGGNTWKSSAANYWKEQIIIEAKGPDVCTPT 194
+G+G D L + ID + ++S G + G A+ G++W S W Q+
Sbjct: 246 HLYGLGIDYLFNFIDNAQKHSSVGFYVGFALAGSSWVGSGGLGMWVSQMDFIN----- 297

Query: 195 YCNP NAPYSTNTSTVAFQVWLNFGVRANIYKHNGVEFGVRVPLLINKFLSAGPNATNLYY 254
N Y T FQ+ LNFGVR N+ +HNG E G+++PL +N F N
Sbjct: 298 --NYLTDYRAKMHTSFFQIPLNFGVRVNVDRHNGFEMGLKIPLAVNSFYETHGKGLNASL 355

Query: 255 HLKRDYSLYLGYN YTF 270
KR + Y Y+F
Sbjct: 356 FFKRLVMFNVS YVYSF 371

tr Q8GDI9 HopQ [HOPQ] [Helicobacter pylori (Campylobacter 641 AA
pylori)] align

Score = 93.6 bits (231), Expect = 3e-18
Identities = 69/211 (32%), Positives = 100/211 (46%), Gaps = 49/211 (23%)

Query: 79 NGALNGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLGKQVYAPNKIQLDMVS 138
 NGALNG G+ GYK+FF K +W G R YG FDY H + + D+ +
 Sbjct: 461 NGALNGLGVQAGYKQFFGQK-----RRW-GLRYYGFFDYNHTYIKSSFF---NSASDVWT 511

Query: 139 WGVGSDLLADIIDKDNASF-----GIFGGVAIGGNTWKSSAANYWKEQIIEAKGPD 189
 +GVGSDLL + I+ N +F G+FGG+A+ G +W +S Q + K
 Sbjct: 512 YGVGSDLLFNFINDKNTNFLGKNNKISVGLFGGIALAGTSWLNS-----QFVNLK--- 561

Query: 190 VCTPTYCNPAPYSTNTSTVAFQVWLNFGVRANIYK-----HNGVEFGVRVPLLI 239
 T N YS +T FQ N G+R N+ + +G+E GV++P +
 Sbjct: 562 ----TISN---VYSAKVNTANFQFLFNGLRTNLRPKKDSHSAQHGMELGVKIPTIN 614

Query: 240 NKFLSAGPNATNLYYHLKRDYSLYLGYNITF 270
 + S T L Y +R YS+YL Y + +
 Sbjct: 615 TNYYSY--LGTKLEY--RRLYSVYLNIVFAY 641

tr Q9S3I7 HopZ protein precursor [HOPZ] [Helicobacter pylori] 666
 (Campylobacter AA
 pylori)] align

Score = 93.2 bits (230), Expect = 4e-18
 Identities = 67/211 (31%), Positives = 102/211 (47%), Gaps = 45/211 (21%)

Query: 75 SKYANGALNGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLGKQVYAPNKIQL 134
 S+ NGA+NG G+ +GYK+FF K +W G R YG FDY HA + +
 Sbjct: 486 SQTNNAMNGIGVQIGYKQFFGEK-----RRW-GLRYYGFFDYNHAYIKSSFF---NSAS 536

Query: 135 DMVSWGVSDDLADIID-----KDNASFGIFGGVAIGGNTWKSSAANYWKEQIIEAKGPD 189
 D+ ++GVG+D+L + I+ + SFG+FGG+A+ G +W +S
 Sbjct: 537 DVFTYGVGTDVLYNFINDKATKNNKISFGVFGGIALAGTSWLNSQY----- 582

Query: 190 VCTPTYCNPAPYSTNTSTVAFQVWLNFGVRANIYKH-----NGVEFGVRVPLLI 239
 V T+ N YS + FQ N G+R N+ K+ +GVE GV++P +
 Sbjct: 583 VNLATF---NNFYSAKMNVANFQFLFNGLRMLAKNKKKASDHAAQHGVELGVKIPTIN 639

Query: 240 NKFLSAGPNATNLYYHLKRDYSLYLGYNITF 270
 + S L Y +R YS+YL Y + +
 Sbjct: 640 TNYISL--LGAQLQY--RRLYSVYLNIVFAY 666

tr Q9ZLB8 Putative outer membrane protein [JHP0662] [Helicobacter pylori] 651
 J99 AA
 (Campylobacter pylori J99)] align

Score = 92.8 bits (229), Expect = 5e-18
 Identities = 72/231 (31%), Positives = 103/231 (44%), Gaps = 52/231 (22%)

Query: 59 LTANKHNPGGTNINWHSKYANGALNGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDY 118
 L A +NP S+ NGALNG G+ VGYK+FF SK +G R YG FDY
 Sbjct: 454 LAAMSNNPFKKVGMISQNNNGALNGLGVQVGYKQFFG-----ESKRWGLRYYGFFDYN 507

Query: 119 HADLGKQVYAPNKIQLDMVSWGVSDDLADIID-----KDNASFGIFGGVAIGGNTWKS 172
 H + + + D+ ++G GSDLL + I+ + S G+FGG+ + G TW +
 Sbjct: 508 HGYIKSSFFNSSS---DIWYGGGSDLLVNFINDSITRKNNKLSVGLFGGIQLAGTTWLN 564

Query: 173 SAANYWKEQIIIEAKGPDVCTPTYCNP---NAPYSTNTSTVAFQVWLNFGVRANI----- 223
 S Y N N PYS + FQ N G+R N+
 Sbjct: 565 S-----QYMNLTAFNNPYSKVNASNQFLFNGLRLTNLATAKKK 604

Query: 224 ----YKHNGVEFGVRVPLLINKFLSAGPNATNLYYHLKRDYSLYLGYNITF 270
 +GVE G+++P + + S T L Y +R YS+YL Y + +
 Sbjct: 605 DSERSAQHGVELGIKIPTINTNYYSF--LGTKLEY--RRLYSVYLNIVFAY 651

tr Q9ZLC1 Putative outer membrane protein [JHP0659] [Helicobacter pylori 638
 J99 AA
 (Campylobacter pylori J99)] align

Score = 92.8 bits (229), Expect = 5e-18
 Identities = 72/231 (31%), Positives = 103/231 (44%), Gaps = 52/231 (22%)

Query: 59 LTANKHNPGGTNINWHSKYANGALNGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDY 118
 L A +NP S+ NGALNG G+ VGYK+FF SK +G R YG FDY
 Sbjct: 441 LAAMSNPNPFKKVGMISQNNNGALNGLGVQVGYKQFFG-----ESKRWGLRYYGFFDYN 494

Query: 119 HADLGKQVYAPNKIQLDMSVSGVSDLLADIID-----KDNASFGIFGGVAIGGNTWKS 172
 H + + + D+ ++G GSDLL + I+ + S G+FGG+ + G TW +
 Sbjct: 495 HGYIKSSFFNSSS---DIWTYGGGSDLLVNFINDSITRKNNKLSVGLFGGIQLAGTTWLN 551

Query: 173 SAANYWKEQIIIEAKGPDVCTPTYCNP---NAPYSTNTSTVAFQVWLNFGVRANI----- 223
 S Y N N PYS + FQ N G+R N+
 Sbjct: 552 S-----QYMNLTAFNNPYSKVNASNQFLFNGLRLTNLATAKKK 591

Query: 224 ----YKHNGVEFGVRVPLLINKFLSAGPNATNLYYHLKRDYSLYLGYNITF 270
 +GVE G+++P + + S T L Y +R YS+YL Y + +
 Sbjct: 592 DSERSAQHGVELGIKIPTINTNYYSF--LGTKLEY--RRLYSVYLNIVFAY 638

tr Q9ZJ82 Putative outer membrane protein [JHP1432] [Helicobacter pylori 242
 J99 AA
 (Campylobacter pylori J99)] align

Score = 92.4 bits (228), Expect = 6e-18
 Identities = 70/278 (25%), Positives = 117/278 (41%), Gaps = 86/278 (30%)

Query: 21 EGDGVYIGTNYQLGQARLNSNIYNTGDCTGSVVGCPPLTANKHNPGGTNINWHSKYANG 80
 +G+GV++G Y GQA++++I N + N
 Sbjct: 23 DGNQVFLGAGYLQQAQMHADI-----NSQKQATNA 53

Query: 81 ALNGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHAD----- 121
 + GF +GY+ FF+ K FG R+YG FDY HA+
 Sbjct: 54 TIKGFDALLGYQFFFE-----KHFGRLRYGFFDYAHANSIKLKNPNYNSEAAQVASQ 105

Query: 122 -LGKQ-----VYAPNKIQLDMSVSGVSDLLADIIDKDNASFGIFGGVAIGGNTWKSS 173
 LGKQ + P + +M+++G D++ ++I+ S G FGG+ + GN+W +
 Sbjct: 106 ILGKQEIINRLTNIADPRTFEPNMLTYGGAMDVMNVINNGIMSLGAFGGIQLAGNSWLMA 165

Query: 174 AANYWKEQIIIEAKGPDVCTPTYCNPAPYSTNTSTVAFQVWLNFGVRANIYKHNGVEFGV 233
 ++ + +A + +FQ N G R I KH+ +E GV

Sbjct: 166 TPSFEGILVEQA-----LVSKKATSFQFLFNVGARLRILKHSSIEAGV 208

Query: 234 RVPLL-INKFLSAGPNATNLYYHLKRDYSLYLGYN YTF 270

+ P+L N +++ A NL +R YS Y+ Y +TF

Sbjct: 209 KFPMLKKNPYIT---AKNLDIGFRRVYSWYVNVYVTF 242

tr Q9ZN38 Putative outer membrane protein [JHP0021] [Helicobacter pylori 690
J99 AA
(Campylobacter pylori J99)] align

Score = 92.0 bits (227), Expect = 8e-18

Identities = 73/248 (29%), Positives = 109/248 (43%), Gaps = 53/248 (21%)

Query: 38 LNSNIYNTGDCTGSVVGCPGLTANKHNPGGTNINWHSKYANGALNGFGLNVGYKKFFQF 97
++SNI++ +G P A TN NGA+NG G VGYK+FF

Sbjct: 481 IDSNIHSQVQSRSQELGSNPFRAGLIAASTTN-----NGAMNGIGFQVGYKQFFG- 531

Query: 98 KSLDMTSKWFGFRVYGLFDYGHADLGKQVYAPNKIQLDMVSWGVSDDLADIID-----K 152
+K +G R YG DY H Q + + D+ ++GVGSDLL + I+

Sbjct: 532 -----KNKRWGARYYGFVDYNHTYNKSQFFNASS---DVWTYGVGSDLLVNFINDKATKH 583

Query: 153 DNASFGIFGGVAIGGNTWKSSAANYWKEQIIEAKGPDVCTPTYCNPAPYSTNTSTVAFQ 212
+ SFG FGG+A+ G +W +S Q + N N Y +T FQ

Sbjct: 584 NKISFGAFGGIALAGTSLWNS-----QYV-----NLANVNYYKAKINTANFQ 626

Query: 213 VWLNFGVRANIYK-----HNGVEFGVRVPLLINKFLSAGPNATNLYYHLKRDYSL 262
N G+R N+ + +G+E G ++P + + S T L Y +R YS+

Sbjct: 627 FLFNLGLRMLNLRKKHRATDNAAQHGIELGTKIPTINTNYYSL--LGTTLQY--RRLYSV 682

Query: 263 YLGYN YTF 270

YL Y + +

Sbjct: 683 YLNYVFAY 690

tr O25945 Hypothetical protein HP1395 [HP1395] [Helicobacter pylori 242 AA
(Campylobacter pylori)] align

Score = 91.7 bits (226), Expect = 1e-17

Identities = 71/278 (25%), Positives = 117/278 (41%), Gaps = 86/278 (30%)

Query: 21 EGDGVYIGTNYQLGQARLNSNIYNTGDCTGSVVGCPGLTANKHNPGGTNINWHSKYANG 80
+G+GV+IG Y GQA+++++I + T + +

Sbjct: 23 DGNVFIGAGYLQGQAQMHADINSQKQATSATI----- 55

Query: 81 ALNGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHAD----- 121
GF +GY+ FF K+FG R+YG FDY HA+

Sbjct: 56 --KGFDALLGYQFFF-----GKYFGLRLYGFFDYAHANSIRLKNPNYNNEVVQLAGQ 105

Query: 122 -LGKQ-----VYAPNKIQLDMVSWGVSDDLADIIDKDNASFGIFGGVAIGGNTWKSS 173
LGKQ + P + +M+++G D++ ++I+ S G FGGV + GN+W +

Sbjct: 106 VLKQKEINRLTSLADPKTFEPNMLTYGGAMDVMVNINNGIMSLGAFGGVQLAGNSWLMA 165

Query: 174 AANYWKEQIIEAKGPDVCTPTYCNPAPYSTNTSTVAFQVWLNFGVRANIYKHNGVEFGV 233


```
      ++      + +A      +      +FQ   N G R   I KH+ +E GV
Sbjct: 166 TPSFEGILVEQA-----LVSKKATSFQFLFNVGARLRILKHSSIEAGV 208

Query: 234 RVPLL-INKFLSAGPNATNLYYHLKRDYSLYLGYN YTF 270
      + P+L   N +++      A NL      +R YS Y+ Y +TF
Sbjct: 209 KFPMLKKNPYIT----AKNLDIGFRRVYSWYVNVVFTF 242
```

tr O25580 **Hypothetical protein HP0923 [HP0923] [Helicobacter pylori 369 AA
(Campylobacter pylori)]**

align

Score = 91.7 bits (226), Expect = 1e-17

Identities = 62/196 (31%), Positives = 91/196 (45%), Gaps = 25/196 (12%)

```
Query: 81  ALNGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLGKQVYAPNKI----QLDM 136
      ++ G   L+VGYK FF   K           K   G R Y   +DYG+ + G   + N           +++
Sbjct: 193 SMYGVSLSVGYKHFFTKK-----KNQGLRYYLFYDYG YTNFG---FVGNGFDGLGKMNN 243

Query: 137 VSWGVSDDLADIID--KDNASFGIFGGVAIGGNTWKSSAANYWKEQIIEAKGPDVCTPT 194
      +G+G D L + ID   K ++S G + G A+ G++W   S   + W   Q           T
Sbjct: 244 HLYGLGIDYLYNFIDNAKKHSSVGFYLG FALAGSSWVGSGLSMWVSQ-----TDF 293

Query: 195 YCNPNAPYSTNTSTVAFQVWLNFGVRANIYKHNGVEFGVRVPLLINKFLSAGPNATNLYY 254
      N   Y           T   FQ+ LNFGVR N+ +HNG E G+++PL +N F           N
Sbjct: 294 INNYLTGYQAKMHTSFFQIPLNFGVRVNVNRHNGFEMGLKIPLAMNSFYETHGKGLNTSL 353

Query: 255 HLKRDYSLYLGYN YTF 270
      KR           + Y Y+F
Sbjct: 354 FFKRLVMFNVS YVYSF 369
```

tr O25222 **Hypothetical protein HP0477 [HP0477] [Helicobacter pylori 367 AA
(Campylobacter pylori)]**

align

Score = 91.7 bits (226), Expect = 1e-17

Identities = 62/196 (31%), Positives = 91/196 (45%), Gaps = 25/196 (12%)

```
Query: 81  ALNGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLGKQVYAPNKI----QLDM 136
      ++ G   L+VGYK FF   K           K   G R Y   +DYG+ + G   + N           +++
Sbjct: 191 SMYGVSLSVGYKHFFTKK-----KNQGLRYYLFYDYG YTNFG---FVGNGFDGLGKMNN 241

Query: 137 VSWGVSDDLADIID--KDNASFGIFGGVAIGGNTWKSSAANYWKEQIIEAKGPDVCTPT 194
      +G+G D L + ID   K ++S G + G A+ G++W   S   + W   Q           T
Sbjct: 242 HLYGLGIDYLYNFIDNAKKHSSVGFYLG FALAGSSWVGSGLSMWVSQ-----TDF 291

Query: 195 YCNPNAPYSTNTSTVAFQVWLNFGVRANIYKHNGVEFGVRVPLLINKFLSAGPNATNLYY 254
      N   Y           T   FQ+ LNFGVR N+ +HNG E G+++PL +N F           N
Sbjct: 292 INNYLTGYQAKMHTSFFQIPLNFGVRVNVNRHNGFEMGLKIPLAMNSFYETHGKGLNTSL 351

Query: 255 HLKRDYSLYLGYN YTF 270
      KR           + Y Y+F
Sbjct: 352 FFKRLVMFNVS YVYSF 367
```

tr 024870 **Hypothetical protein HP0025 [HP0025] [Helicobacter pylori 711 AA
(Campylobacter pylori)]**

align

Score = 90.9 bits (224), Expect = 2e-17

Identities = 73/248 (29%), Positives = 110/248 (43%), Gaps = 53/248 (21%)

Query: 38 LNSNIYNTGDC TGSVVGCPPGLTANKHNPGGTNINWHSKYANGALNGFGLNVGYKKFFQF 97
++SNI++ +G P A TN NGA+NG G VGYK+FF
Sbjct: 502 IDSNIHSQVQSR SQELGSNPFRRAGLIAASTTN-----NGAMNGIGFQVGYKQFFG- 552

Query: 98 KSLDMTSKWFGFRVYGLFDYGHADLGKQVYAPNKIQLDMVSWGVSDDLADIID-----K 152
+K +G R YG DY H Q + + D+ ++GVGSDLL + I+
Sbjct: 553 -----KNKRWGARYYGFVDYNHTYNKSQFFNSDS---DVWTYGVGSDLLVNFINDKATKH 604

Query: 153 DNASF G I F G G V A I G G N T W K S S A A N Y W K E Q I I E A K G P D V C T P T Y C N P N A P Y S T N T S T V A F Q 212
+ SFG FGG+ + G +W +S Q + N N Y +T FQ
Sbjct: 605 NKISFGAFGGIQLAGT SWLNS-----QYV-----NLANVNNYYKAKINTSNFQ 647

Query: 213 VWLNFGVRANIYKH-----NGVEFGVRVPLLINKFLSAGPNATNLYYHLKRDYSL 262
N G+R N+ ++ +G+E GV++P + + S T L Y +R YS+
Sbjct: 648 FLFNLGLRTNLARNKRIGADHSAQHGMELGVKIPTINTNYYSL--LGTTLQY--RRLYSV 703

Query: 263 YLGYN YTF 270

YL Y + +

Sbjct: 704 YLNYVFAY 711

tr Q9ZK57 **Putative outer membrane protein [JHP1084] [Helicobacter 1237
pylori J99 AA
(Campylobacter pylori J99)]**

align

Score = 90.1 bits (222), Expect = 3e-17

Identities = 68/208 (32%), Positives = 103/208 (48%), Gaps = 52/208 (25%)

Query: 79 NGALNGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLGKQVYAPNKIQLDMVS 138
+G NG G+ +GYK FF ++ G R Y FDYG +++G A ++ ++ +
Sbjct: 1058 HGMSNGLGVGIGYKYFFG-----KARKLGLRHYFFFDYGFSEIG---LANQSVKANIFA 1108

Query: 139 WGVGSDLLADIIDKDN----ASFGIFGGVAIGGNTWKSSAANYWKEQIIIEAKGPDVCTPT 194
+GVG+D L ++ + +FG+F GV +GG TW SS ++QII+ G
Sbjct: 1109 YGVGTDFLWNLFRRTYNTKALNFGFLFAGVQLGGATWLSSL----RQQIIDNWG----- 1157

Query: 195 YCNPNAPYSTNTSTVAFQVWLNFGVRAN-----IYKHNGVEFGVRVPLLI 239
N N +STN FQV LNFGVR N + VEEG++VPL+
Sbjct: 1158 --NANDIHSTN-----FQVALNFGVRTNFAEFKRFKAKKFHNQGVISQKSVEFGIKVPLIN 1210

Query: 240 NKFL-SAGPNATNLYYHLKRDYSLYLYG 266

+L SAG + + +R Y+ Y+ Y

Sbjct: 1211 QAYLNSAGADVS-----YRRLYTFYINY 1233

tr Q93HU1 **HPOMP29(SS1) protein [HPOMP29(SS1)] [Helicobacter 260 AA
pylori align]**

(Campylobacter pylori)]

Score = 90.1 bits (222), Expect = 3e-17

Identities = 73/265 (27%), Positives = 112/265 (41%), Gaps = 37/265 (13%)

Query: 21 EGDGVYIGTNYQLGQAR-----LNSNIYNTGDCTGSVVGCPPGLTANKHNPGGTNI 71
 E G ++G +Q N+N GS P + P N

Sbjct: 18 EKSGAFLGGGFQYSNLENQNTTRTPGANNNTPIDTSMFGSNQTAPAPQAQATYTPSVINT 77

Query: 72 NWSKYANGALNGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADL---GKQV-Y 127
 N + G + G GYK FF +K FGFR YG + Y HA+L G Q+

Sbjct: 78 NNY-----GQMYGVDAMAGYKWFFG-----KTKRFGFRSYGYYSYNHANLSFVGSQGLGI 126

Query: 128 APNKIQLDMVSWGVGSDLLADIIDKDNA--SFGIFGGVAIGGNTWKSSAANYWKEQIIEA 185
 Q++ ++GVG D L + + + G+F G +GG+T+ +Y K Q+

Sbjct: 127 MEGASQVNNFTYGVGFDALYNFYESKEGYNTAGLFLGFLGGDTFIVQGESYLKSQM--- 183

Query: 186 KGPDVCTPTYCNPAPYSTNTSTVAFQVWLNFGVRANIYKHNGVEFGVRVPLLINKFLSA 245
 CN A S + +T FQ+ + FG R+N KH+G+E G ++PL N+F

Sbjct: 184 -----HVCNNTAGCSASMNTSYFQMPVEFGFRSNFSKHSGIEVGFKLPLFTNQFYKE 235

Query: 246 GPNATNLYYHLKRDYSLYLGNYTF 270
 ++ KR++S+Y Y F

Sbjct: 236 RGVDGSVDVIFYKRNFYSIFYNYMINF 260

tr Q93HU0 **OMU116 protein [OMU116] [Helicobacter pylori (Campylobacter pylori)]**

align

Score = 89.0 bits (219), Expect = 7e-17

Identities = 71/265 (26%), Positives = 110/265 (40%), Gaps = 37/265 (13%)

Query: 21 EGDGVYIGTNYQLGQAR-----LNSNIYNTGDCTGSVVGCPPGLTANKHNPGGTNI 71
 E G ++G +Q N+N GS P + P N

Sbjct: 18 EKSGAFLGGGFQYSNLESQNTTRTPGANNNTPIDTSMFGSNQTAPAPQAQATYTPSVINT 77

Query: 72 NWSKYANGALNGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLG----KQVY 127
 N + G + G GYK FF +K FGFR YG + Y HA+L K

Sbjct: 78 NNY-----GQMYGVDAMAGYKWFFG-----KTKRFGFRSYGYYSYNHANLSFVGSKLGI 126

Query: 128 APNKIQLDMVSWGVGSDLLADIIDKDNA--SFGIFGGVAIGGNTWKSSAANYWKEQIIEA 185
 Q++ ++GVG D L + + + G+F G +GG+++ +Y K Q+

Sbjct: 127 MEGASQVNNFTYGVGFDALYNFYESKEGYNTAGLFLGFLGGDSFVVQGESYLKSQM--- 183

Query: 186 KGPDVCTPTYCNPAPYSTNTSTVAFQVWLNFGVRANIYKHNGVEFGVRVPLLINKFLSA 245
 CN A S + +T FQ+ + FG R+N KH+G+E G ++PL N+F

Sbjct: 184 -----QICNNTAGCSASMNTSYFQMPVEFGFRSNFSKHSGIEVGFKLPLFTNQFYEE 235

Query: 246 GPNATNLYYHLKRDYSLYLGNYTF 270
 ++ KR++S+Y Y F

Sbjct: 236 RGVDGSVDVIFYKRNFYSIFYNYMINF 260

tr Q9ZMI2 **Putative outer membrane protein [JHP0238] [Helicobacter pylori 471**

J99
(Campylobacter pylori J99)]

AA
align

Score = 88.6 bits (218), Expect = 9e-17
 Identities = 64/209 (30%), Positives = 97/209 (45%), Gaps = 50/209 (23%)

Query: 79 NGALNGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLGKQVYAPNKIQLDMVS 138
 +G +NGFG+ VGYK+FF K K G R Y FDYG LG + ++ ++ +
 Sbjct: 296 HGVINGFGIQVGYKQFFGSK-----KNIGLRYYAFFDYGFTQLGS---LNSAVKANIFT 346

Query: 139 WGVGSDLLADIIDK---DNASFGIFGGVAIGGNTWKSSAANYWKEQIEAKGPDVCTPT 194
 +G G+D L +I + + + G+FGG+ I GNTW SS IE + TPT
 Sbjct: 347 YGAGTDFLWNIFRRVFSDDQSLNVGVFGGIQIAGNTWDSSLRGQ-----IENSFKEYPTPT 401

Query: 195 YCNPNAPYSTNTSTVAFQVWLNFGVRANIYK-----HNGVEFGVRVPLLINK 241
 FQ N G+RA+ +G+EFGV++P + +
 Sbjct: 402 -----NFQFLFNGLRAHFASTMHRRLSASQSIQHGMFVGKIPAINQR 446

Query: 242 FLSAGPNATNLYYHLKRDYSLYLGNYTF 270
 +L A N ++ Y +R Y+ Y+ Y F
 Sbjct: 447 YLKA--NGADVDY--RRLYAFYINYTIGF 471

tr O24908 **Hypothetical protein HP0079 [HP0079] [Helicobacter pylori 595 AA**
(Campylobacter pylori)]

align

Score = 88.6 bits (218), Expect = 9e-17
 Identities = 60/197 (30%), Positives = 95/197 (47%), Gaps = 23/197 (11%)

Query: 80 GALNGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADL---GKQV-YAPNKIQLD 135
 G + G GYK FF +K FGFR YG + Y HA+L G Q+ Q++
 Sbjct: 416 GQMYGVDAMAGYKWFFG-----KTKRFGFRSYGYYSYNHANLSFVGSQLGIMEGASQVN 469

Query: 136 MVSWGVSDDLADIIDKDNA--SFGIFGGVAIGGNTWKSSAANYWKEQIEAKGPDVCTP 193
 ++GVG D+L + + + G+F G +GG+++ +Y K Q+
 Sbjct: 470 NFTYGVGFVDVLYNFYESKEGYNTAGLFLGFLGGDSFIVQGESYLKSQM----- 518

Query: 194 TYCNPNAPYSTNTSTVAFQVWLNFGVRANIYKHNGVEFGVRVPLLINKFLSAGPNATNLY 253
 CN A S + +T FQ+ + FG R+N KH+G+E G ++PL N+F ++
 Sbjct: 519 HICNNTAGCSASMNTSYFQMPVEFGFRSNFSKHSIEVGFKLPLFTNQFYKERGVDSVD 578

Query: 254 YHLKRDYSLYLGNYTF 270
 KR++S+Y Y F
 Sbjct: 579 VFYKRNFYSIFYNYMINF 595

tr Q93HU2 **HPomp29(43504) protein [HPOMP29(43504)] [Helicobacter pylori 255 AA**
(Campylobacter pylori)]

align

Score = 88.6 bits (218), Expect = 9e-17
 Identities = 69/256 (26%), Positives = 112/256 (42%), Gaps = 24/256 (9%)

Query: 21 EGDGVYIGTNYQLGQARLNSNIYNTGDCTGSVVGCPPLTANKHNPGGTNINWHISKYANG 80

```

      E  G  ++G  +Q      N  N  T      +      +N+  P      +  +      G
Sbjct: 18  EKSGAFLGGGFQYSNLE-NQNTTRTPGANNNTPIDTSMFGSNQVAPAQETPSVINTNNYG 76

Query: 81  ALNGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADL---GKQV-YAPNKIQLDM 136
      +  G      GYK  FF      +K  FGFR  YG  +  Y  HA+L      G  Q+      Q++
Sbjct: 77  QMYGVDAMAGYKWFFG-----KTKRFGFRSYGYYSYNHANLSFVGSQGLGIMEGASQVND 130

Query: 137 VSWGVGSDLLADIIDKDNA--SFGIFGGVAIGGNTWKSSAANYWKEQIIEAKGPDVCTPT 194
      ++GVG  D+L  +  +      +  G+F  G  +GG+++      +Y  K  Q+
Sbjct: 131 FTYGVGFVDVLYNFYESKEGYNTAGLFLGFLGGDSFIVQGESYLKSQM-----H 179

Query: 195 YCNP NAPYSTNTSTVAFQVWLNFGVRANIYKHNGVEFGVRVPLLINKFLSAGPNATNLYY 254
      CN  A  S  +  +T  FQ+  +  FG  R+N  KH+G+E  G  ++PL  N+F      ++
Sbjct: 180 ICNNTAGCSASMNTSYFQMPVEFGFRSNFSKHSIEVGFKLPLFTNQFYKERGVGDGSVDV 239

Query: 255 HLKRDYSLYLGYN YTF 270
      KR++S+Y  Y  F
Sbjct: 240 FYKRNFSIYFN YMINF 255

```

tr O25091 **Hypothetical protein HP0324 [HP0324] [Helicobacter pylori 254 AA (Campylobacter pylori)]**

align

Score = 88.2 bits (217), Expect = 1e-16

Identities = 72/254 (28%), Positives = 110/254 (42%), Gaps = 49/254 (19%)

```

Query: 25  VYIGTNYQLGQARLNSNIYNTGDCTGSSVVGCPGLTANKHNPGGTNINWHSKYANGALNG 84
      +Y+G NYQ  G  L  +NI+  +  T  G  +T+      +N  K  N  NG
Sbjct: 42  LYMGVNYQTGSINLMTNIHEVREVTNYQTGYTNIITS-----VNSVKKLTNMGSNG 92

Query: 85  FGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLG--KQVYAPNKIQLDMVSWGVG 142
      GL  +GY  FF      K  G  R  +  D+      +  K  Y  N  +M+++GVG
Sbjct: 93  IGLVMGYNHFFH-----PDKILGLRYFAFLDWQGYGMRYPKGYGGN----NMITYGVG 142

Query: 143 SDLLADII-----DKDNASFGIFGGVAIGGNTWKSSAANYWKEQIIEAKGPDVCTPTYC 196
      D  +  +      D  +  G+FGG+AI  GN+W      I  +KG  ++  T
Sbjct: 143 VDAVWNFFQGSFYQDDISVDIGVFGGIAIAGNSW-----YIGSKGQELLGIT-- 189

Query: 197 NPNAPYSTNTSTVAFQVWLNFGVRANIYKHNGVEFGVRVPLLINKFLSAGPNATNLYYHL 256
      N+  NTS  FQ  NFG++A  +  E  G  +  P  +  NK+  +      L  +
Sbjct: 190 --NSSAVDNTS---FQFLFNFGGLKALFVDEHEFEIGFKFPTINNKYTTDA----LKVQM 240

Query: 257 KRDYSLYLGYN YTF 270
      +R  ++  Y+GYNY  F
Sbjct: 241 RRVFAFYVGYN YHF 254

```

tr Q9ZMY9 **Putative outer membrane protein [JHP0073] [Helicobacter pylori 255 AA (Campylobacter pylori J99)]**

align

Score = 87.8 bits (216), Expect = 2e-16

Identities = 58/193 (30%), Positives = 91/193 (47%), Gaps = 23/193 (11%)

Query: 80 GALNGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLG----KQVYAPNKIQLD 135
 G + G GYK FF +K FGFR YG + Y HA+L K Q++
 Sbjct: 76 GQMYGVDAMAGYKWWFFG-----KTKRFGFRTYGYYSYNHANLSFVGSGLGIMDGASQVN 129

Query: 136 MVSWSGSDLLADIIDKDNA--SFGIFGGVAIGGNTWKSSAANYWKEQIIIEAKGPDVCTP 193
 ++GVG D L + + + G+F G +GG+++ +Y K Q+
 Sbjct: 130 NFTYGVGFDALYNFYESKEGYNTAGLFVGFGLGGDSFIVQGESYLKSQM----- 178

Query: 194 TYCNP NAPYSTNTSTVAFQVWLNFGVRANIYKHNGVEFGVRVPLLINKFLSAGPNATNLY 253
 CN A S + +T FQ+ + FG R+N KH+G+E G ++PL N+F ++
 Sbjct: 179 QICNNTAGCSASMNTSYFQMPVEFGFRSNFSKHSIEVGFKLPLFTNQFYKERGVDSVD 238

Query: 254 YHLKRDYSLYLG Y 266
 KR++S+Y Y
 Sbjct: 239 VFYKRNFYSIYFNY 251

tr 025772 **Hypothetical protein HP1157 [HP1157] [Helicobacter pylori** 1230 AA
pylori align
(Campylobacter pylori)]

Score = 87.4 bits (215), Expect = 2e-16
 Identities = 67/208 (32%), Positives = 103/208 (49%), Gaps = 52/208 (25%)

Query: 79 NGALNGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLGKQVYAPNKIQLD MVS 138
 +G NG G+ +GYK FF ++ G R Y FDYG +++G A ++ ++ +
 Sbjct: 1051 HGMSNGLGVGLGYKYFFG-----KARKLGLRHYFFFDYGFSEIG---LANQSVKANIFA 1101

Query: 139 WGVGSDLLADIIDKDN----ASFGIFGGVAIGGNTWKSSAANYWKEQIIIEAKGPDVCTPT 194
 +GVG+D L ++ + +FG+F GV +GG TW SS ++QII+ G
 Sbjct: 1102 YGVGTDFLWNLFRRTYNTKALNFGLFAGVQLGGATWLSSL----RQQIIDNWG----- 1150

Query: 195 YCNP NAPYSTNTSTVAFQVWLNFGVRAN-----IYKHNGVEFGVRVPLLI 239
 + N +STN FQV LNFGVR N + VEFG++VPL+
 Sbjct: 1151 --SANDIHSTN-----FQVALNFGVRTNFAEFKRFKKFHNQGVISQKSVEFGIKVPLIN 1203

Query: 240 NKFL-SAGPNATNLYYHLKRDYSLYLG Y 266
 +L SAG + + +R Y+ Y+ Y
 Sbjct: 1204 QAYLNSAGADVS-----YRRLYTFYINY 1226

tr Q9X751 **HopX protein precursor [HOPX] [Helicobacter pylori** 472
(Campylobacter AA
pylori)] align

Score = 87.4 bits (215), Expect = 2e-16
 Identities = 63/209 (30%), Positives = 97/209 (46%), Gaps = 50/209 (23%)

Query: 79 NGALNGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLGKQVYAPNKIQLD MVS 138
 +G +NGFG+ VGYK+FF K + G R Y FDYG LG + ++ ++ +
 Sbjct: 297 HGVINGFGIQVGYKQFFGSK-----RNIGLRYAFFDYGFTQLGS---LNSAVKANIFT 347

Query: 139 WGVGSDLLADIIDK---DNASFGIFGGVAIGGNTWKSSAANYWKEQIIIEAKGPDVCTPT 194
 +G G+D L +I + + +G+FGG+ I GNTW SS IE + TPT
 Sbjct: 348 YGAGTDFLWNIFRRVFSDQSLNVGVFGGIQIAGNTWDSSLRGQ-----IENSFKEYPTPT 402

```

Query: 195 YCNPNAPYSTNTSTVAFQVWLNFGVRANIYK-----HNGVEFGVRVPLLINK 241
              FQ   N G+RA+                      +G+EFGV+ +P  +  +
Sbjct: 403 -----NFQFLFNLGLRAHFASTMHRRFLSSSQSIQHGMFEFGVKIPAINQR 447

Query: 242 FLSAGPNATNLYYHLKRDYSLYLGYN YTF 270
              +L A  N  ++ Y  +R Y+ Y+ Y   F
Sbjct: 448 YLKA--NGADVDY--RRLYAFYINYTIGF 472

```

tr	<u>Q9ZMB4</u>	Putative outer membrane protein [JHP0307] [Helicobacter pylori J99 (Campylobacter pylori J99)]	245 AA align
----	---------------	--	--------------------

Score = 87.0 bits (214), Expect = 3e-16
Identities = 74/254 (29%), Positives = 107/254 (41%), Gaps = 49/254 (19%)

Query: 25 VYIGTNYQLGQARLNSNIYNTGDCTGSVVGCPGLTANKHNPGGTNINWHSKYANGALNG 84
+Y+G NYQ G L +NI+ + T G +T+ IN K N NG
Sbjct: 33 LYMGFNYQTGSINLMANIHEVREVTSYQTGYTNVMTS-----INSVKKLTNMGSGNG 83

Query: 85 FGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLG--KQVYAPNKIQLDMVSWGVG 142
GL +GY FF K G R + D+ + K Y N +M+++GVG
Sbjct: 84 IGLVMGYNHFFH-----PDKVLGLRYFAFLDWOGYGMRYPKGYYGGN---NMITYGVG 133

```

Query: 143 SDLLADII-----DKDNASFGIFGGVAIGGNTWKSSAANYWKEQIIIEAKGPDVCTPTYC 196
          D + +          D          G+FGG+AI GN+W          I  KG ++   T
Sbjct: 134 VDAIWNFFQGSFYQDDIGVDIGVFGGIAIAGNSW-----YIGNKGOELLGIT-- 180

```

Query: 197 NPNAPYSTNTSTVAFQVWLNFGVRANIYKHNGVEFGVRVPLLINKFLSAGPNATNLYYHL 256
N+ NTS FQ NFG +A + E G + P L NK+ + L +
Sbjct: 181 --NSSAVDNTS---FQFLNFGFKALFVDEHEFEIGFKFPTLNNKYYTTDA----LKVQM 231

Query: 257 KRDYSLYLGYN YTF 270
+R ++ Y+G YNY F
Sbjct: 232 RRVFAFYVGYNYHF 245

```
tr 025036 Outer membrane protein (OMP8) [HP0254] [Helicobacter pylori 431 AA  
(Campylobacter pylori)]  
align
```

Score = 87.0 bits (214), Expect = 3e-16
Identities = 63/209 (30%), Positives = 97/209 (46%), Gaps = 50/209 (23%)

Query: 79 NGALNGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLGKQVYAPNKKIQLDMVS 138
+G +NGFG+ VGYK+FF K + G R Y FDYG LG + ++ ++ +
Sbjct: 256 HGVINGFGIQVGYKOFFGKNK-----RNIGLRYAFFDYGFTOLGS---LSSAVKANIFT 306

Query: 139 WGVGSDLLADIIDK----DNASFGIFGGVAIGGNTWKSSAANYWKEQIIIEAKGPDVCTPT 194
+G G+D L +I + + + G+FGG+ I GNTW SS IE + TPT
Sbjct: 307 YGAGTDFLWNIFRRRVFSDQSLNVGVFGGIIQIAGNTWDSSLRGO-----IENSFKEYPTPT 361

Query: 195 YCNPNAPYSTNTSTVAFQVVLNFGVRANIYK-----HNGVEFGVRVPLLINK 241
 FQ. N G+RA+ +G+EFQV++P + +

Sbjct: 362 -----NFQFLFNLGLRAHFASTMHRRFLSASQSIQHGMFEGVKIPAINQR 406

Query: 242 FLSAGPNATNLYYHLKRDYSLYLGNYTF 270
 +L A N ++ Y +R Y+ Y+ Y F

Sbjct: 407 YLRA--NGADVDY--RRLYAFYINYTIGF 431

tr Q9X749 **HopV protein precursor (27 kDa outer membrane protein) [HOPV] 248 AA**
[Helicobacter pylori (Campylobacter pylori)]

align

Score = 87.0 bits (214), Expect = 3e-16
 Identities = 67/273 (24%), Positives = 110/273 (39%), Gaps = 73/273 (26%)

Query: 21 EGDGVYIGTNYQLGQARLNSNIYNTGDCTGSVVGCPPGLTANKHNPGGTNINWHSKYANG 80
 E ++G NYQ+ + + + N ++ PP YA

Sbjct: 18 EESAAPVGVNYQVSMIQNQTKMVNDNGLQKPLIKFPP-----YA-- 56

Query: 81 ALNGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGH-----ADLGKQVYAPNK 131
 G G VGYK+FF K KWFG R YG FDY H +G+ + N

Sbjct: 57 ---GAGFEVGYKQFFGKK-----KWFGARYYGFFDYAHNRFGVMKKGIPVGESGFIYNS 107

Query: 132 IQ-----LDMVSWGVSDDLADIIDKDNASFGIFGGVAIGGNTWKSSA 174
 +++ ++GVG D L + ++K+N FG G+ + G++W +S

Sbjct: 108 FSFGGNTLMERDSYQGQYYVNLFTYGVGLDTLWNFVNKENMVFGEFVVGIIQLAGDSWATSI 167

Query: 175 ANYWKEQIIIEAKGPDVCTPTYCNPAPYSTNTSTVAFQVWLNFGVRANIYKHNGVEFGVR 234
 + ++ + + N+ Y S FQ FGVR +I KHN +E G++

Sbjct: 168 SK-----EIASYAKHHSNSSY---SPANFQFLWKFGVRTHIAKHNSLELGIIK 211

Query: 235 VPLLINKFLS-AGPNATNLYYHLKRDYSLYLG 266
 VP + ++ S L ++R Y+ + Y

Sbjct: 212 VPTITHRLFSLTNEKGYTLQADVRRVYAFQISY 244

tr O26005 **Hypothetical protein HP1469 [HP1469] [Helicobacter pylori 248 AA**
(Campylobacter pylori)]

align

Score = 86.3 bits (212), Expect = 5e-16
 Identities = 71/273 (26%), Positives = 110/273 (40%), Gaps = 73/273 (26%)

Query: 21 EGDGVYIGTNYQLGQARLNSNIYNTGDCTGSVVGCPPGLTANKHNPGGTNINWHSKYANG 80
 E ++G NYQ+ + + + N ++ PP YA

Sbjct: 18 EESAAPVGVNYQVSMIQNQTKMVNDNGLQKPLIKFPP-----YA-- 56

Query: 81 ALNGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLGKQ-----VYAP 129
 G G VGYK+FF K KWFG R YG FDY H G +Y

Sbjct: 57 ---GAGFEVGYKQFFGKK-----KWFGMRYYGFFDYAHNRFGVMKKGIPVGDSGFIYNS 107

Query: 130 -----NKIQDLMVSWGVSDDLADIIDKDNASFGIFGGVAIGGNTWKSSA 174
 + +++ ++GVG D L + ++K+N FG G+ + G++W +S

Sbjct: 108 FSFGGNTLTERDSYQGQYYVNLFTYGVGLDTLWNFVNKENMVFGEFVVGIIQLAGDSWATSI 167

Query: 175 ANYWKEQIIIEAKGPDVCTPTYCNPAPYSTNTSTVAFQVWLNFGVRANIYKHNGVEFGVR 234


```
      +   KE   AK           + N+ Y   S   FQ   FGVR +I KHN +E G++
Sbjct: 168 S---KEIAHYAKH-----HSNSSY----SPANFQFLWKFGVVRTHIAKHNSLELGIIK 211

Query: 235 VPLLINKFLS-AGPNATNLYYHLKRDYSLYLGY 266
      VP + ++ S           L   ++R Y+   + Y
Sbjct: 212 VPTITHQLFSLTNEKGYTLQADVRRVYAFQISY 244
```

tr Q9ZJY3 Outer membrane protein-adhesin [BABB] [Helicobacter pylori J99 703 AA
(Campylobacter pylori J99)]

align

Score = 85.9 bits (211), Expect = 6e-16
Identities = 75/267 (28%), Positives = 113/267 (42%), Gaps = 71/267 (26%)

```
Query: 27  IGTNYQLGQARLNSNIYNTGDCTGSVVGCPP---GLTANKHNPGGTNINWHSKYANGAL 82
      I TNY L       N N YN           +G P   G+ +++ N           NGA+
Sbjct: 485 IDTNYYL-----NQNSYNQIQTINQELGRNPFRKVGIVSSQTN-----NGAM 526

Query: 83  NGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLGKQVYAPNKIQLDMVSWSVG 142
      NG G+ VGYK+FF K           KW G R YG FDY HA +   +   D+ ++G G
Sbjct: 527 NGIGIQVGYKQFFGQK-----RKW-GARYYGFFDYNHAFIKSSFF---NSASDVWTYGF 577

Query: 143 SDLLADIID-----KDNASFGIFGGVAIGGNTWKSSAANYWKEQIIIEAKGPDVCTP 193
      +D L + I+           + S G+FGG+A+ G +W +S           E +
Sbjct: 578 ADALYNFINDKATNFLGKNNKLSVGLFGGIALAGTSWLNS-----EYV----- 620

Query: 194 TYCNP NAPYSTNTSTVA FQVWLNFGVRANIYK-----HNGVEFGVRVPLLINKFL 243
      N Y+   +   FQ   N GVR N+ +           +G+E G+++P +   +
Sbjct: 621 NLATMNNVYNAMNANVFQFLFNMGVRMNLARPKKSDHAAQHGIELGLKIPTINTNY 680

Query: 244 SAGPNATNLYYHLKRDYSLYLGYNYTF 270
      S           L Y   +R YS+YL Y + +
Sbjct: 681 SF--MGAELKY--RRLYSVYLYNVFAY 703
```

tr Q9ZKV2 Outer membrane protein-adhesin [BABA] [Helicobacter pylori J99 744 AA
(Campylobacter pylori J99)]

align

Score = 85.9 bits (211), Expect = 6e-16
Identities = 75/267 (28%), Positives = 113/267 (42%), Gaps = 71/267 (26%)

```
Query: 27  IGTNYQLGQARLNSNIYNTGDCTGSVVGCPP---GLTANKHNPGGTNINWHSKYANGAL 82
      I TNY L       N N YN           +G P   G+ +++ N           NGA+
Sbjct: 526 IDTNYYL-----NQNSYNQIQTINQELGRNPFRKVGIVSSQTN-----NGAM 567

Query: 83  NGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLGKQVYAPNKIQLDMVSWSVG 142
      NG G+ VGYK+FF K           KW G R YG FDY HA +   +   D+ ++G G
Sbjct: 568 NGIGIQVGYKQFFGQK-----RKW-GARYYGFFDYNHAFIKSSFF---NSASDVWTYGF 618

Query: 143 SDLLADIID-----KDNASFGIFGGVAIGGNTWKSSAANYWKEQIIIEAKGPDVCTP 193
      +D L + I+           + S G+FGG+A+ G +W +S           E +
Sbjct: 619 ADALYNFINDKATNFLGKNNKLSVGLFGGIALAGTSWLNS-----EYV----- 661
```

Query: 194 TYCNPAPYSTNTSTVAFQVWLNFGVRANIYK-----HNGVEFGVRVPLLINKFL 243
 N Y+ + FQ N GVR N+ + +G+E G+++P + +
 Sbjct: 662 NLATMNNVYNAKMNVANFQFLFNMGVRMNLARPKKKSDHAAQHGIELGLKIPTINTNY 721

Query: 244 SAGPNATNLYYHLKRDYSLYLGNYTF 270
 S L Y +R YS+YL Y + +
 Sbjct: 722 SF--MGAEELKY--RRLYSVYLNLYVFAY 744

tr O34523 Hypothetical protein HP1342 [HP1342] [Helicobacter pylori 691 AA
 (Campylobacter pylori)]

align

Score = 85.9 bits (211), Expect = 6e-16
 Identities = 63/211 (29%), Positives = 97/211 (45%), Gaps = 49/211 (23%)

Query: 79 NGALNGFGLNVGYKKFFQPKSLDMTSKWFGFRVYGLFDYGHADLGKQVYAPNKIQLDMVS 138
 NGA+NG G+ VGYK+FF K + +G R YG FDY HA + + D+ +
 Sbjct: 511 NGAMNGIGVQVGYKQFFGKK-----RNWGLRYYGFFDYNHAYIKSNFF---NSASDVWT 561

Query: 139 WGVGSDLLADIIDKDNASF-----GIFGGVAIGGNTWKSSAANYWKEQIIEAKGPD 189
 +GVG D L + I+ N +F G+FGG A+ G +W +S +Q+
 Sbjct: 562 YGVGMDALYNFINDKNTNFLGKNNKLSVGLFGGFALAGTSLWLS-----QQV----- 608

Query: 190 VCTPTYCNPAPYSTNTSTVAFQVWLNFGVRANIYK-----HNGVEFGVRVPLLI 239
 N Y+ N ST FQ + G+R N+ + +G+E G ++P + +
 Sbjct: 609 ----NLTMNGIYNANVSTSNFQFLFDLGLRMNLARPKKKSDHAAQHGIELGFKIPTIN 664

Query: 240 NKFLSAGPNATNLYYHLKRDYSLYLGNYTF 270
 + S L Y +R YSL+L Y + +
 Sbjct: 665 TNYYSF--MGAKLEY--RRMYSLFLNYVFAY 691

tr Q9ZK58 Putative outer membrane protein [JHP1083] [Helicobacter pylori 697
 J99 AA
 (Campylobacter pylori J99)]

align

Score = 85.5 bits (210), Expect = 8e-16
 Identities = 56/210 (26%), Positives = 98/210 (46%), Gaps = 48/210 (22%)

Query: 74 HSKYANGALNGFGLNVGYKKFFQPKSLDMTSKWFGFRVYGLFDYGHADLGKQVYAPNKIQ 133
 H+ +N +NGFG+ +GYK+FF K + FG R YG +D+G+A G + + ++
 Sbjct: 523 HNSNSNN-MNGFGVKMGYKQFFGKKRM-----FGLRYYGFYDFGYAQFGTE---SSLVK 572

Query: 134 LDMVSWGVSDDLADIIDKDNAS----FGIFGGVAIGGNTWKSSAANYWKEQIIEAKGPD 189
 + S+G G+D L ++ + + G F G+ + G TWK++ + ++ K
 Sbjct: 573 ATLSSYGAGTDFLYNVFTRKRGTEAIDIGFFAGIQLAGQTWKTNFLDQVDGNHLKPK--- 629

Query: 190 VCTPTYCNPAPYSTNTSTVAFQVWLNFGVRANIYK-----HNGVEFGVRVPLLIN 240
 +FQ + G+R N K G+EFG+++P+L +
 Sbjct: 630 -----DTSFQFLFDLGIRTNFSKIAHQKRSRFSQGIEFGLKIPVLYH 671

Query: 241 KFLSAGPNATNLYYHLKRDYSLYLGNYTF 270
 + + T Y +RD+S Y+GYN F
 Sbjct: 672 TYYQS-EGVTAKY---RRDFSFYVGYNIGF 697

tr 025086 Outer membrane protein (OMP9) [HP0317] [Helicobacter pylori 745 AA
(Campylobacter pylori)]

align

Score = 85.5 bits (210), Expect = 8e-16

Identities = 75/263 (28%), Positives = 110/263 (41%), Gaps = 63/263 (23%)

Query: 27 IGTNYQLGQARLNSNIYNTGDCTGSVVGCPPGLTANKHNPGGTNINWHSKYANGALNGFG 86
I TNY L N N YN +G P N S+ NGA+NG G
Sbjct: 527 IETNYYL-----NQNSYNQIQTINQELGRNPFRKVGIVN-----SQTNNGAMNGIG 572

Query: 87 LNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLGKQVYAPNKIQLDMVSWGVSDDL 146
+ VGYK+FF K KW G R YG FDY HA + + D+ ++G G+D L
Sbjct: 573 IQVGYKQFFGQK-----RKW-GARYYGFFDYNHAFIKSSFF---NSASDVWTYGFGADAL 623

Query: 147 ADIID-----KDNASFGIFGGVAIGGNTWKSSAANYWKEQIIEAKGPDVCTPTYCN 197
+ I+ + S G+FGG+A+ G +W +S E +
Sbjct: 624 YNFINDKATNFLGKNNKLSLGLFGGIALAGTSWLNS-----EYV-----NLAT 666

Query: 198 PNAPYSTNTSTVAFQVWLNFGVRANIYK-----HNGVEFGVRVPLLINKFLSAGP 247
N Y+ + FQ N GVR N+ + +G+E G+++P + + S
Sbjct: 667 VNNVYNAKMNVANFQFLFNMGVRMNLARSKKKGSDHAAQHGIELGLKIPTINTNYYSF-- 724

Query: 248 NATNLYYHLKRDYSLYLGNYTF 270
L Y +R YS+YL Y + +
Sbjct: 725 MGAELKY--RRLYSVYLNLYVFAY 745

tr 025840 Hypothetical protein HP1243 [HP1243] [Helicobacter pylori 733 AA
(Campylobacter pylori)]

align

Score = 85.5 bits (210), Expect = 8e-16

Identities = 75/263 (28%), Positives = 110/263 (41%), Gaps = 63/263 (23%)

Query: 27 IGTNYQLGQARLNSNIYNTGDCTGSVVGCPPGLTANKHNPGGTNINWHSKYANGALNGFG 86
I TNY L N N YN +G P N S+ NGA+NG G
Sbjct: 515 IETNYYL-----NQNSYNQIQTINQELGRNPFRKVGIVN-----SQTNNGAMNGIG 560

Query: 87 LNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLGKQVYAPNKIQLDMVSWGVSDDL 146
+ VGYK+FF K KW G R YG FDY HA + + D+ ++G G+D L
Sbjct: 561 IQVGYKQFFGQK-----RKW-GARYYGFFDYNHAFIKSSFF---NSASDVWTYGFGADAL 611

Query: 147 ADIID-----KDNASFGIFGGVAIGGNTWKSSAANYWKEQIIEAKGPDVCTPTYCN 197
+ I+ + S G+FGG+A+ G +W +S E +
Sbjct: 612 YNFINDKATNFLGKNNKLSLGLFGGIALAGTSWLNS-----EYV-----NLAT 654

Query: 198 PNAPYSTNTSTVAFQVWLNFGVRANIYK-----HNGVEFGVRVPLLINKFLSAGP 247
N Y+ + FQ N GVR N+ + +G+E G+++P + + S
Sbjct: 655 VNNVYNAKMNVANFQFLFNMGVRMNLARSKKKGSDHAAQHGIELGLKIPTINTNYYSF-- 712

Query: 248 NATNLYYHLKRDYSLYLGNYTF 270
L Y +R YS+YL Y + +

Sbjct: 713 MGAELKY--RRLYSVYLNIVFAY 733

tr Q9R7I4 Adhesin-binding fucosylated histo-blood group antigen [BABA1] 703 AA
[Helicobacter pylori (Campylobacter pylori)]

align

Score = 85.5 bits (210), Expect = 8e-16

Identities = 75/267 (28%), Positives = 113/267 (42%), Gaps = 71/267 (26%)

Query: 27 IGTNYQLGQARLNSNIYNTGDCTGSVVGCP-----GLTANKHNPGGTNINWHSKYANGAL 82
I TNY L N N YN +G P G+ +++ N NGA+
Sbjct: 485 IETNYYL-----NQNSYNQIQITINQELGRNPFRKVGIVSSQTN-----NGAM 526

Query: 83 NGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLGKQVYAPNKIQLDMVSWSVG 142
NG G+ VGYK+FF K KW G R YG FDY HA + + D+ ++G G
Sbjct: 527 NGIGIQVGYKQFFGQK-----RKW-GARYYGFFDYNHAFIKSSFF---NSASDVWTYGFG 577

Query: 143 SDLLADIID-----KDNASFGIFGGVAIGNTWKSSAANYWKEQIEAKGPDVCTP 193
+D L + I+ + S G+FGG+A+ G +W +S E +
Sbjct: 578 ADALYNFINDKATNFLGKNNKLSVGLFGGIALAGTSLWLS-----EYV----- 620

Query: 194 TYCNPAPYSTNTSTVAFQVWLNFGVRANIYK-----HNGVEFGVRVPLLINKFL 243
N Y+ + FQ N GVR N+ + +G+E G+++P + +
Sbjct: 621 NLATMNNVYNAKMNVANFQFLFMGVRMNLARSKKKGSDHAAQHGIELGLKIPTINTNYY 680

Query: 244 SAGPNATNLYYHLKRDYSLYLGNYTF 270
S L Y +R YS+YL Y + +
Sbjct: 681 SF--MGAELKY--RRLYSVYLNIVFAY 703

tr O51811 Adhesin-binding fucosylated histo-blood group antigen [BABB] 707 AA
[Helicobacter pylori (Campylobacter pylori)]

align

Score = 85.5 bits (210), Expect = 8e-16

Identities = 75/267 (28%), Positives = 113/267 (42%), Gaps = 71/267 (26%)

Query: 27 IGTNYQLGQARLNSNIYNTGDCTGSVVGCP-----GLTANKHNPGGTNINWHSKYANGAL 82
I TNY L N N YN +G P G+ +++ N NGA+
Sbjct: 489 IETNYYL-----NQNSYNQIQITINQELGRNPFRKVGIVSSQTN-----NGAM 530

Query: 83 NGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLGKQVYAPNKIQLDMVSWSVG 142
NG G+ VGYK+FF K KW G R YG FDY HA + + D+ ++G G
Sbjct: 531 NGIGIQVGYKQFFGQK-----RKW-GARYYGFFDYNHAFIKSSFF---NSASDVWTYGFG 581

Query: 143 SDLLADIID-----KDNASFGIFGGVAIGNTWKSSAANYWKEQIEAKGPDVCTP 193
+D L + I+ + S G+FGG+A+ G +W +S E +
Sbjct: 582 ADALYNFINDKATNFLGKNNKLSVGLFGGIALAGTSLWLS-----EYV----- 624

Query: 194 TYCNPAPYSTNTSTVAFQVWLNFGVRANIYK-----HNGVEFGVRVPLLINKFL 243
N Y+ + FQ N GVR N+ + +G+E G+++P + +
Sbjct: 625 NLATMNNVYNAKMNVANFQFLFMGVRMNLARSKKKGSDHAAQHGIELGLKIPTINTNYY 684

Query: 244 SAGPNATNLYYHLKRDYSLYLGNYTF 270

S L Y +R YS+YL Y + +
 Sbjct: 685 SF--MGAELKY--RRLYSVYLNLYVFAY 707

tr 052269 Adhesin binding fucosylated histo-blood group antigen [BABA2] 741 AA
 [Helicobacter pylori (Campylobacter pylori)]

align

Score = 85.5 bits (210), Expect = 8e-16
 Identities = 75/267 (28%), Positives = 113/267 (42%), Gaps = 71/267 (26%)

Query: 27 IGTNYQLGQARLNSNIYNTGDCTGSVVGCPP----GLTANKHNPGGTNINWHSKYANGAL 82
 I TNY L N N YN +G P G+ +++ N NGA+
 Sbjct: 523 IETNYYL-----NQNSYNQIQ TINQELGRNPFRKVGIVSSQTN-----NGAM 564

Query: 83 NGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLGKQVYAPNKIQLDMVSWG VG 142
 NG G+ VGYK+FF K KW G R YG FDY HA + + D+ ++G G
 Sbjct: 565 NGIGIQVGYKQFFGQK-----RKW-GARYYGFFDYNHAFIKSSFF---NSASDVWTYGF G 615

Query: 143 SDLLADIID-----KDNASFGIFGGVAIGGNTWKSSAANYWKEQIIEAKGPDVCTP 193
 +D L + I+ + S G+FGG+A+ G +W +S E +
 Sbjct: 616 ADALYNFINDKATNFLGKNNKLSVGLFGGIALAGT SWLNS-----EYV----- 658

Query: 194 TYCNP NAPYSTNTSTVAFQVWLNFGVRANIYK-----HNGVEFGVRVPLLINKFL 243
 N Y+ + FQ N GVR N+ + +G+E G+++P + +
 Sbjct: 659 NLATMNNVYNAKMNVANFQFLFNMGVRMNLARSKKKGS DHAAQHGIELGLKIPTINTNYY 718

Query: 244 SAGPNATNLYYHLKRDYSLYLGYN YTF 270
 S L Y +R YS+YL Y + +
 Sbjct: 719 SF--MGAELKY--RRLYSVYLNLYVFAY 741

trnew AAR95689 BabA [Helicobacter pylori (Campylobacter pylori)] 742 AA
align

Score = 85.5 bits (210), Expect = 8e-16
 Identities = 75/267 (28%), Positives = 113/267 (42%), Gaps = 71/267 (26%)

Query: 27 IGTNYQLGQARLNSNIYNTGDCTGSVVGCPP----GLTANKHNPGGTNINWHSKYANGAL 82
 I TNY L N N YN +G P G+ +++ N NGA+
 Sbjct: 524 IETNYYL-----NQNSYNQIQ TINQELGRNPFRKVGIVSSQTN-----NGAM 565

Query: 83 NGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLGKQVYAPNKIQLDMVSWG VG 142
 NG G+ VGYK+FF K KW G R YG FDY HA + + D+ ++G G
 Sbjct: 566 NGIGIQVGYKQFFGQK-----RKW-GARYYGFFDYNHAFIKSSFF---NSASDVWTYGF G 616

Query: 143 SDLLADIID-----KDNASFGIFGGVAIGGNTWKSSAANYWKEQIIEAKGPDVCTP 193
 +D L + I+ + S G+FGG+A+ G +W +S E +
 Sbjct: 617 ADALYNFINDKATNFLGKNNKLSVGLFGGIALAGT SWLNS-----EYV----- 659

Query: 194 TYCNP NAPYSTNTSTVAFQVWLNFGVRANIYK-----HNGVEFGVRVPLLINKFL 243
 N Y+ + FQ N GVR N+ + +G+E G+++P + +
 Sbjct: 660 NLATMNNVYNAKMNVANFQFLFNMGVRMNLARPKKSDHAAQHGIELGLKIPTINTNYY 719

Query: 244 SAGPNATNLYYHLKRDYSLYLGYN YTF 270

S L Y +R YS+YL Y + +
Sbjct: 720 SF--MGAELKY--RRLYSVYLYNYVFAY 742

trnew AAR95688 BabB2 [Helicobacter pylori (Campylobacter 706 AA
pylori)] align

Score = 85.5 bits (210), Expect = 8e-16
Identities = 75/267 (28%), Positives = 113/267 (42%), Gaps = 71/267 (26%)

Query: 27 IGTNYQLGQARLNSNIYNTGDCTGSVVGCPP----GLTANKHNPGGTNINWHSKYANGAL 82
I TNY L N N YN +G P G+ +++ N NGA+
Sbjct: 488 IETNYYL-----NQNSYNQIQITINQELGRNPFRKVGIVSSQTN-----NGAM 529

Query: 83 NGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLGKQVYAPNKIQLDMSVSWGVG 142
NG G+ VGYK+FF K KW G R YG FDY HA + + D+ ++G G
Sbjct: 530 NGIGIQVGYKQFFGQK-----RKW-GARYYGFFDYNHAFIKSSFF---NSASDVWTYGFG 580

Query: 143 SDLLADIID-----KDNASFGIFGGVAIGGNTWKSSAANYWKEQIIEAKGPDVCTP 193
+D L + I+ + S G+FGG+A+ G +W +S E +
Sbjct: 581 ADALYNFINDKATNFLGKNNKLSVGLFGGIALAGTSWLNS-----EYV----- 623

Query: 194 TYCNP NAPYSTNTSTVAFQVWLNFGVRANIYK-----HNGVEFGVRVPLLINKFL 243
N Y+ + FQ N GVR N+ + +G+E G+++P + +
Sbjct: 624 NLATMNNVYNAKMNVANFQFLFMGVRMNLARPKKKSDHAAQHGIELGLKIPTINTNY 683

Query: 244 SAGPNATNLYYHLKRDYSLYLGNYTF 270
S L Y +R YS+YL Y + +
Sbjct: 684 SF--MGAELKY--RRLYSVYLYNYVFAY 706

trnew AAR95687 BabB [Helicobacter pylori (Campylobacter 706 AA
pylori)] align

Score = 85.5 bits (210), Expect = 8e-16
Identities = 75/267 (28%), Positives = 113/267 (42%), Gaps = 71/267 (26%)

Query: 27 IGTNYQLGQARLNSNIYNTGDCTGSVVGCPP----GLTANKHNPGGTNINWHSKYANGAL 82
I TNY L N N YN +G P G+ +++ N NGA+
Sbjct: 488 IETNYYL-----NQNSYNQIQITINQELGRNPFRKVGIVSSQTN-----NGAM 529

Query: 83 NGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLGKQVYAPNKIQLDMSVSWGVG 142
NG G+ VGYK+FF K KW G R YG FDY HA + + D+ ++G G
Sbjct: 530 NGIGIQVGYKQFFGQK-----RKW-GARYYGFFDYNHAFIKSSFF---NSASDVWTYGFG 580

Query: 143 SDLLADIID-----KDNASFGIFGGVAIGGNTWKSSAANYWKEQIIEAKGPDVCTP 193
+D L + I+ + S G+FGG+A+ G +W +S E +
Sbjct: 581 ADALYNFINDKATNFLGKNNKLSVGLFGGIALAGTSWLNS-----EYV----- 623

Query: 194 TYCNP NAPYSTNTSTVAFQVWLNFGVRANIYK-----HNGVEFGVRVPLLINKFL 243
N Y+ + FQ N GVR N+ + +G+E G+++P + +
Sbjct: 624 NLATMNNVYNAKMNVANFQFLFMGVRMNLARPKKKSDHAAQHGIELGLKIPTINTNY 683

Query: 244 SAGPNATNLYYHLKRDYSLYLGNYTF 270
S L Y +R YS+YL Y + +

Sbjct: 684 SF--MGAELKY--RRLYSVYLNLYVFAY 706

trnew AAR95686 **BabB [Helicobacter pylori (Campylobacter pylori)]** 706 AA
align

Score = 85.5 bits (210), Expect = 8e-16

Identities = 75/267 (28%), Positives = 113/267 (42%), Gaps = 71/267 (26%)

Query: 27 IGTNYQLGQARLNSNIYNTGDCTGSVVGCPP----GLTANKHNPGGTNINWHSKYANGAL 82
I TNY L N N YN +G P G+ +++ N NGA+

Sbjct: 488 IETNYYL-----NQNSYNQIQITINQELGRNPFRKVGIVSSQTN-----NGAM 529

Query: 83 NGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLGKQVYAPNKIQLDMVSWGVG 142
NG G+ VGYK+FF K KW G R YG FDY HA + + D+ ++G G

Sbjct: 530 NGIGIQVGYKQFFGQK-----RKW-GARYYGFFDYNHAFIKSSFF---NSASDVWTYGF 580

Query: 143 SDLLADIID-----KDNASFGIFGGVAIGGNTWKSSAANYWKEQIIEAKGPDVCTP 193
+D L + I+ + S G+FGG+A+ G +W +S E +

Sbjct: 581 ADALYNFINDKATNFLGKNNKLSVGLFGGIALAGTSLWLS-----EYV----- 623

Query: 194 TYCNPAPYSTNTSTVAFQVWLNFGVRANIYK-----HNGVEFGVRVPLLINKFL 243
N Y+ + FQ N GVR N+ + +G+E G+++P + +

Sbjct: 624 NLATMNNVYNAKMNVANFQFLFNMGVRMNLARPKKSDHAAQHGIELGLKIPTINTNY 683

Query: 244 SAGPNATNLYYHLKRDYSLYLGYN YTF 270

S L Y +R YS+YL Y + +

Sbjct: 684 SF--MGAELKY--RRLYSVYLNLYVFAY 706

tr 025556 **Outer membrane protein (OMP19) [HP0896] [Helicobacter pylori (Campylobacter pylori)]** 708 AA
align

Score = 85.1 bits (209), Expect = 1e-15

Identities = 75/263 (28%), Positives = 110/263 (41%), Gaps = 63/263 (23%)

Query: 27 IGTNYQLGQARLNSNIYNTGDCTGSVVGCPGLTANKHNPGGTNINWHSKYANGALNGFG 86
I TNY L N N YN +G P N S+ NGA+NG G

Sbjct: 490 IETNYYL-----NQNSYNQIQITINQELGRNPFRKVGIVN-----SQTNNGAMNGIG 535

Query: 87 LNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLGKQVYAPNKIQLDMVSWGVGSDLL 146
+ VGYK+FF K KW G R YG FDY HA + + D+ ++G G+D L

Sbjct: 536 IQVGYKQFFGQK-----RKW-GARYYGFFDYNHAFIKSSFF---NSASDVWTYGF 586

Query: 147 ADIID-----KDNASFGIFGGVAIGGNTWKSSAANYWKEQIIEAKGPDVCTPTYCN 197
+ I+ + S G+FGG+A+ G +W +S E +

Sbjct: 587 YNFINDKATNFLGKNNKLSVGLFGGIALAGTSLWLS-----EYV-----NLAT 629

Query: 198 PNAPYSTNTSTVAFQVWLNFGVRANIYK-----HNGVEFGVRVPLLINKFLSAGP 247
N Y+ + FQ N GVR N+ + +G+E G+++P + + S

Sbjct: 630 VNNVYNAKMNVANFQFLFNMGVRMNLARSKKKSDHAAQHGIELGLKIPTINTNYYSF-- 687

Query: 248 NATNLYYHLKRDYSLYLGYN YTF 270

L Y +R YS+YL Y + +

Sbjct: 688 MGAELKY--RRLYSVYLNIVFAY 708

tr Q7WV97 **Adhesin-binding fucosylated histo-blood group antigen** 694
 (Fragment) AA
 [BABB] [*Helicobacter pylori* (*Campylobacter pylori*)] align

Score = 84.3 bits (207), Expect = 2e-15

Identities = 77/257 (29%), Positives = 109/257 (41%), Gaps = 63/257 (24%)

Query: 27 IGTNYQLGQARLNSNIYNTGDCTGSVVGCPGLTANKHNPGGTNINWHSKYANGALNGFG 86
 I TNY L N N YN +G P K G+ N NGA+NG G

Sbjct: 481 IETNYYL-----NQNSYNQIQITINQELGRNP---FRKVGIVGSQTN-----NGAMNGIG 526

Query: 87 LNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLGKQVYAPNKIQLDMVSWGVSDDL 146
 + VGYK+FF K KW G R YG FDY HA + + D+ ++G G+D L

Sbjct: 527 IQVGYKQFFGQK-----RKW-GARYYGFFDYNHAFIKSSFF---NSASDVWTYGFGADAL 577

Query: 147 ADIID-----KDNASFGIFGGVAIGGNTWKSSAANYWKEQIIEAKGPDVCTPTYCN 197
 + I+ + S G+FGG+A+ G +W +S E +

Sbjct: 578 YNFINDKATNFLGKNNKLSVGLFGGIALAGTSWLNS-----EYV-----NLAT 620

Query: 198 PNAPYSTNTSTVAFQVWLNFGVRANIYK-----HNGVEFGVRVPLLINKFLSAGP 247
 N Y+ +T FQ N GVR N+ + +G+E GV++P + + S

Sbjct: 621 VNNVYNKINTANFQFLFMGMVRMNLARAKKKGSDHAAQHGIELGVKIPTINTNYYSF-- 678

Query: 248 NATNLYYHLKRDYSLYL 264

L Y +R YS+YL

Sbjct: 679 MGAELKY--RRLYSVYL 693

tr Q9Z390 **Putative outer membrane protein [JHP0212] [*Helicobacter pylori* 696
 J99 AA
 (*Campylobacter pylori* J99)] align**

Score = 83.2 bits (204), Expect = 4e-15

Identities = 62/211 (29%), Positives = 96/211 (45%), Gaps = 49/211 (23%)

Query: 79 NGALNGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLGKQVYAPNKIQLDMVS 138
 NGA+NG G+ GYK+FF K + +G R YG FDY HA + + D+ +

Sbjct: 516 NGAMNGIGVQAGYKQFFGKK-----RNWGLRYYGFFDYNHAYIKSNFF---NSASDVWT 566

Query: 139 WGVGSDLLADIIDKDNASF-----GIFGGVAIGGNTWKSSAANYWKEQIIEAKGPD 189
 +GVG D L + I+ N +F G+FGG A+ G +W +S +Q+

Sbjct: 567 YGVGMDALYNFINDKNTNFLGKNNKLSVGLFGGFALAGTSWLNS-----QQV----- 613

Query: 190 VCTPTYCNPAPYSTNTSTVAFQVWLNFGVRANIYK-----HNGVEFGVRVPLLI 239
 N Y+ N S FQ + G+R N+ + +G+E GV++P +

Sbjct: 614 ---NLTMMNGIYNANVSASNFQFLFDLGLRMNLARPKKKSDHAAQHGMELGVKIPTIN 669

Query: 240 NKFLSAGPNATNLYYHLKRDYSLYLGNYTF 270

+ S L Y +R YS+YL Y + +

Sbjct: 670 TDYYSF--MGAELKY--RRLYSVYLNIVFAY 696

tr Q7WV70 Adhesin-binding fucosylated histo-blood group antigen 733
(Fragment) AA
[BABB] [Helicobacter pylori (Campylobacter pylori)] align

Score = 83.2 bits (204), Expect = 4e-15
Identities = 75/260 (28%), Positives = 110/260 (41%), Gaps = 71/260 (27%)

Query: 27 IGTNYQLGQARLNSNIYNTGDCTGSVVGCPP---GLTANKHNPGGTNINWHSKYANGAL 82
I TNY L N N YN +G P G+ +++ N NGA+
Sbjct: 522 IETNYYL-----NQNSYNQIQITINQELGRNPFRKVGIVSSQTN-----NGAM 563

Query: 83 NGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLGKQVYAPNKIQLDMVSWGVG 142
NG G+ VGYK+FF K KW G R YG FDY HA + + D+ ++G G
Sbjct: 564 NGIGIQVGYKQFFGQK-----RKW-GARYYGFFDYNHAFIKSSFF---NSASDVWTYGF 614

Query: 143 SDLLADIID-----KDNASFGIFGGVAIGGNTWKSSAANYWKEQIIIEAKGPDVCTP 193
+D L + I+ + S G+FGG+A+ G +W +S E +
Sbjct: 615 ADALYNFINDKATNFLGKNNKLSVGLFGGIALAGTSLWLS-----EYV----- 657

Query: 194 TYCNPAPYSTNTSTVAFQVWLNFGVRANIYK-----HNGVEFGVRVPLLINKFL 243
N Y+ +T FQ N GVR N+ + +G+E GV++P + +
Sbjct: 658 NLATVNNVYNAKINTANFQFLFMGVRMNLARAKKKGSDHAAQHGIELGVKIPTINTNYY 717

Query: 244 SAGPNATNLYYHLKRDYSLY 263
S L Y +R YS+Y
Sbjct: 718 SF--MGAELKY--RRLYSVY 733

tr Q7WV86 Adhesin-binding fucosylated histo-blood group antigen 704
(Fragment) AA
[BABB] [Helicobacter pylori (Campylobacter pylori)] align

Score = 83.2 bits (204), Expect = 4e-15
Identities = 73/261 (27%), Positives = 111/261 (41%), Gaps = 71/261 (27%)

Query: 27 IGTNYQLGQARLNSNIYNTGDCTGSVVGCPP---GLTANKHNPGGTNINWHSKYANGAL 82
I TNY L N N YN +G P G+ +++ N NGA+
Sbjct: 491 IETNYYL-----NPNAYNQIQITINQELGRNPFRKVGIVSSQTN-----NGAM 532

Query: 83 NGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLGKQVYAPNKIQLDMVSWGVG 142
NG G+ +GYK+FF K + +G R YG FDY HA + + D+ ++GVG
Sbjct: 533 NGIGVQMGYKQFFGKK-----RNWGLRYYGFFDYNHAFIKSSFF---NSASDVWTYGVG 583

Query: 143 SDLLADIIDKDNASF-----GIFGGVAIGGNTWKSSAANYWKEQIIIEAKGPDVCTP 193
D L + I+ N +F G+FGG+A+ G +W +S E +
Sbjct: 584 MDALYNFINDKNTNFLGKNNKLSVGLFGGIALAGTSLWLS-----EYV----- 626

Query: 194 TYCNPAPYSTNTSTVAFQVWLNFGVRANIYK-----HNGVEFGVRVPLLINKFL 243
N Y+ + FQ N GVR N+ + +G+E G+++P + +
Sbjct: 627 NLATVNNVYNAKMNVANFQFLFMGVRMNLARSKKKGSDHAAQHGIELGLKIPTINTNYY 686

Query: 244 SAGPNATNLYYHLKRDYSLYL 264
S L Y +R YS+YL
Sbjct: 687 SF--MGAELKY--RRLYSVYL 703

tr Q7WV90 **Adhesin-binding fucosylated histo-blood group antigen** 697
(Fragment) AA
[BABB] [*Helicobacter pylori* (*Campylobacter pylori*)] align

Score = 83.2 bits (204), Expect = 4e-15
Identities = 74/261 (28%), Positives = 109/261 (41%), Gaps = 71/261 (27%)

Query: 27 IGTNYQLGQARLNSNIYNTGDCTGSVVGCPP----GLTANKHNPGGTNINWHSKYANGAL 82
I TNY L N N YN +G P G+ +++ N NGA+
Sbjct: 484 IETNYYL-----NQNSYNQIQITINQELGRNPFRKMGISSQTN-----NGAM 525

Query: 83 NGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLGKQVYAPNKIQLDMSWVG 142
NG G+ VGYK+FF K +W G R YG FDY HA + + D+ ++G G
Sbjct: 526 NGIGIQVGYKQFFGQK-----RRW-GARYYGGFDYNHAFIKSSFF---NSASDVWTYGF 576

Query: 143 SDLLADIID-----KDNASFGIFGGVAIGGNTWKSSAANYWKEQIIIEAKGPDVCTP 193
+D L + I+ + S G+FGG+A+ G +W +S
Sbjct: 577 ADALYNFINDKATNFLGKNNKLSVGLFGGIALAGTSLWLNSE-----FV 619

Query: 194 TYCNPAPYSTNTSTVAFQVWLNFGVRANIYK-----HNGVEFGVRVPLLINKFL 243
N Y+ +T FQ N GVR N+ + +G+E GV++P + +
Sbjct: 620 NLATVNNVYNAKINTANFQFLFNMGVRMNLARAKKGSDHAAQHGIELGVKIPTINTNYY 679

Query: 244 SAGPNATNLYYHLKRDYSLYL 264
S L Y +R YS+YL
Sbjct: 680 SF--MGAELKY--RRLYSVYL 696

tr Q7WV96 **Adhesin-binding fucosylated histo-blood group antigen** 694
(Fragment) AA
[BABB] [*Helicobacter pylori* (*Campylobacter pylori*)] align

Score = 83.2 bits (204), Expect = 4e-15
Identities = 75/261 (28%), Positives = 111/261 (41%), Gaps = 71/261 (27%)

Query: 27 IGTNYQLGQARLNSNIYNTGDCTGSVVGCPP----GLTANKHNPGGTNINWHSKYANGAL 82
I TNY L N N YN +G P G+ +++ N NGA+
Sbjct: 481 IETNYYL-----NQNNYNQIQITINQELGRNPFRKMGISSQTN-----NGAM 522

Query: 83 NGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLGKQVYAPNKIQLDMSWVG 142
NG G+ VGYK+FF K KW G R YG FDY HA + + D+ ++G G
Sbjct: 523 NGIGIQVGYKQFFGQK-----RKW-GARYYGGFDYNHAFIKSSFF---NSASDVWTYGF 573

Query: 143 SDLLADIID-----KDNASFGIFGGVAIGGNTWKSSAANYWKEQIIIEAKGPDVCTP 193
+D L + I+ + S G+FGG+A+ G +W +S E +
Sbjct: 574 ADALYNFINDKATNFLGKNNKLSVGLFGGIALAGTSLWLNSE-----EYV----- 616

Query: 194 TYCNPAPYSTNTSTVAFQVWLNFGVRANIYK-----HNGVEFGVRVPLLINKFL 243
N Y+ +T FQ N G+R N+ + +G+E GV++P + +
Sbjct: 617 NLATVNNVYNAKINTANFQFLFNLGLRMNLARAKKGSDHAAQHGIELGVKIPTINTNYY 676

Query: 244 SAGPNATNLYYHLKRDYSLYL 264
S L Y +R YS+YL
Sbjct: 677 SF--MGAELKY--RRLYSVYL 693

tr Q7WV91 Adhesin-binding fucosylated histo-blood group antigen 696
(Fragment) AA
[BABB] [Helicobacter pylori (Campylobacter pylori)] align

Score = 82.8 bits (203), Expect = 5e-15
Identities = 74/261 (28%), Positives = 111/261 (42%), Gaps = 71/261 (27%)

Query: 27 IG TNYQLGQARLNSNIYNTGDCTGSVVGCPP----GLTANKHNPGGTNINWHSKYANGAL 82
I TNY L N N YN +G P G+ +++ N NGA+
Sbjct: 483 IETNYYL-----NQNSYNQVQTINQELGRNPFRKMGIVSSQTN-----NGAM 524

Query: 83 NGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLGKQVYAPNKIQLDMVSWGVG 142
NG G+ VGYK+FF K +W G R YG FDY HA + + D+ ++G G
Sbjct: 525 NGIGIQVGYKQFFGQK-----RRW-GARYYGFFDYNHAFIKSNFF--NSASDVWTYGF 575

Query: 143 SDLLADIID-----KDNASFGIFGGVAIGGNTWKSSAANYWKEQIIIEAKGPDVCTP 193
+D L + I+ + S G+FGG+A+ G +W +S E +
Sbjct: 576 ADALYNFINDKATNFLGKNNKLSVGLFGGIALAGTSLWLS-----EYV----- 618

Query: 194 TYCNP NAPYSTNTSTVAFQVWLNFGVRANIYK-----HNGVEFGVRVPLLINKFL 243
N Y+ +T FQ N G+R N+ + +G+E GV++P + +
Sbjct: 619 NLATVNNVYNAKINTANFQFLFNGLRMNLARAKKKGSDHAAQHGIELGVKIPTINTNYY 678

Query: 244 SAGPNATNLYYHLKRDYSLYL 264
S L Y +R YS+YL
Sbjct: 679 SF--MGAELKY--RRLYSVYL 695

tr Q7WV94 Adhesin-binding fucosylated histo-blood group antigen 695
(Fragment) AA
[BABB] [Helicobacter pylori (Campylobacter pylori)] align

Score = 82.8 bits (203), Expect = 5e-15
Identities = 75/261 (28%), Positives = 110/261 (41%), Gaps = 71/261 (27%)

Query: 27 IG TNYQLGQARLNSNIYNTGDCTGSVVGCPP----GLTANKHNPGGTNINWHSKYANGAL 82
I TNY L N N YN +G P G+ +++ N NGA+
Sbjct: 482 IETNYYL-----NQNSYNQIQITINQELGRNPFRKVGIVSSQTN-----NGAM 523

Query: 83 NGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLGKQVYAPNKIQLDMVSWGVG 142
NG G+ VGYK+FF K KW G R YG FDY HA + + D+ ++G G
Sbjct: 524 NGIGIQVGYKQFFGQK-----RKW-GARYYGFFDYNHAFIKSSFF--NSASDVWTYGF 574

Query: 143 SDLLADIID-----KDNASFGIFGGVAIGGNTWKSSAANYWKEQIIIEAKGPDVCTP 193
+D L + I+ + S G+FGG+A+ G +W +S E +
Sbjct: 575 ADALYNFINDKATNFLGKNNKLSVGLFGGIALAGTSLWLS-----EYV----- 617

Query: 194 TYCNP NAPYSTNTSTVAFQVWLNFGVRANIYK-----HNGVEFGVRVPLLINKFL 243
N Y+ + FQ N GVR N+ + +G+E GV++P + +
Sbjct: 618 NLATVNNVYNAKMNVANFQFLFNMGVRMNLARSKKKGSDHAAQHGIELGVKIPTINTNYY 677

Query: 244 SAGPNATNLYYHLKRDYSLYL 264
S L Y +R YS+YL
Sbjct: 678 SF--MGAELKY--RRLYSVYL 694

tr Q7WV95 **Adhesin-binding fucosylated histo-blood group antigen** 695
(Fragment) AA
[BABB] [*Helicobacter pylori* (*Campylobacter pylori*)] align

Score = 82.8 bits (203), Expect = 5e-15
Identities = 76/257 (29%), Positives = 108/257 (41%), Gaps = 63/257 (24%)

Query: 27 IGTNYQLGQARLNSNIYNTGDC TGSVVGCPGLTANKHNPGGTNINWHSKYANGALNGFG 86
I TNY L N N YN +G P K G+ N NGA+NG G
Sbjct: 482 IETNYYL-----NQNSYNQVQTINQELGRNP---FRKVGIVGSQTN-----NGAMNGIG 527

Query: 87 LNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLGKQVYAPNKIQLDMVSWGVSDDL 146
+ VGYK+FF K KW G R YG FDY HA + + D+ ++G G+D L
Sbjct: 528 IQVGYKQFFGQK-----RKW-GARYYGFFDYNHAFIKSSFF---NSASDVWTYGFGADAL 578

Query: 147 ADIID-----KDNASFGIFGGVAIGGNTWKSSAANYWKEQIIIEAKGPDVCTPTYCN 197
+ I+ + S G+FGG+A+ G +W +S E +
Sbjct: 579 YNFINDKATNFLGKNNKLSVGLFGGIALAGTSWLNS-----EYV-----NLAT 621

Query: 198 PNAPYSTNTSTVAFQVWLNFGVRANIYK-----HNGVEFGVRVPLLINKFLSAGP 247
N Y+ + FQ N GVR N+ + +G+E GV++P + + S
Sbjct: 622 VNNVYNAKMNVANFQFLFNMGVRMNLARAKKKGSDHAAQHGIELGVKIPTINTNYYSF-- 679

Query: 248 NATNLYYHLKRDYSLYL 264
L Y +R YS+YL
Sbjct: 680 MGAELKY--RRLYSVYL 694

tr Q7WVA3 **Adhesin-binding fucosylated histo-blood group antigen** 694
(Fragment) AA
[BABB] [*Helicobacter pylori* (*Campylobacter pylori*)] align

Score = 82.8 bits (203), Expect = 5e-15
Identities = 76/257 (29%), Positives = 108/257 (41%), Gaps = 63/257 (24%)

Query: 27 IGTNYQLGQARLNSNIYNTGDC TGSVVGCPGLTANKHNPGGTNINWHSKYANGALNGFG 86
I TNY L N N YN +G P K G+ N NGA+NG G
Sbjct: 481 IETNYYL-----NQNTYNQIQITINQELGRNP---FRKVGIVGSQTN-----NGAMNGIG 526

Query: 87 LNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLGKQVYAPNKIQLDMVSWGVSDDL 146
+ VGYK+FF K KW G R YG FDY HA + + D+ ++G G+D L
Sbjct: 527 IQVGYKQFFGQK-----RKW-GARYYGFFDYNHAFIKSSFF---NSASDVWTYGFGADAL 577

Query: 147 ADIID-----KDNASFGIFGGVAIGGNTWKSSAANYWKEQIIIEAKGPDVCTPTYCN 197
+ I+ + S G+FGG+A+ G +W +S E +
Sbjct: 578 YNFINDKATNFLGKNNKLSVGLFGGIALAGTSWLNS-----EYV-----NLAT 620

Query: 198 PNAPYSTNTSTVAFQVWLNFGVRANIYK-----HNGVEFGVRVPLLINKFLSAGP 247
N Y+ + FQ N GVR N+ + +G+E GV++P + + S
Sbjct: 621 VNNVYNAKMNAANFQFLFNMGVRMNLARPKKSDHAAQHGIELGVKIPTINTNYYSF-- 678

Query: 248 NATNLYYHLKRDYSLYL 264
L Y +R YS+YL
Sbjct: 679 MGAELKY--RRLYSVYL 693

tr Q25771 **Hypothetical protein HP1156 [HP1156] [Helicobacter pylori 696 AA
(Campylobacter pylori)]**

align

Score = 82.4 bits (202), Expect = 7e-15

Identities = 55/210 (26%), Positives = 97/210 (46%), Gaps = 48/210 (22%)

Query: 74 HSKYANGALNGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLGKQVYAPNKIQ 133
H+ +N +NGFG+ +GYK+FF K + FG R YG +D+G+A G + + ++
Sbjct: 522 HNSNSNN-MNGFGVKMGYKQFFGKKRM-----FGLRYYGFYDFGYAQFGAE---SSLVK 571

Query: 134 LDMVSWGVSDDLADIIDKDNAS----FGIFGGVAIGGNTWKSSAANYWKEQIIEAKGPD 189
+ S+G G+D L ++ + + G F G+ + G TWK++ + ++ K
Sbjct: 572 ATLSSYGAGTDFLYNVFTRKRGTEAIDIGFFAGIQLAGQTWKTNFLDQVDGNHLKPK--- 628

Query: 190 VCTPTYCNPAPYSTNTSTVAFQVWLNFGVRANIYK-----HNGVEFGVRVPLLIN 240
+FQ + G+R N K G+EFG+++P+L +
Sbjct: 629 -----DTSFQFLFDLGIRTNFSKIAHQKRSRFSQGIEFGLKIPVLYH 670

Query: 241 KFLSAGPNATNLYYHLKRDYSLYLGYN YTF 270
+ + T Y +R +S Y+GYN F
Sbjct: 671 TYYQS-EGVTAKY---RRAFSFYVGYNIGF 696

tr Q7WV89 **Adhesin-binding fucosylated histo-blood group antigen
(Fragment)
[BABB] [Helicobacter pylori (Campylobacter pylori)]**

697

AA

align

Score = 82.4 bits (202), Expect = 7e-15

Identities = 74/261 (28%), Positives = 111/261 (42%), Gaps = 71/261 (27%)

Query: 27 IGTNYQLGQARLNSNIYNTGDCTGSVVGCPP----GLTANKHNPGGTNINWHSKYANGAL 82
I TNY L N N YN +G P G+ +++ N NGA+
Sbjct: 484 IETNYYL----NQNSYNQIQITINQELGRNPFRKMGI VSSQTN-----NGAM 525

Query: 83 NGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLGKQVYAPNKIQ LDMVSWGVS 142
NG G+ VGYK+FF K +W G R YG FDY HA + + D+ ++G G
Sbjct: 526 NGIGIQVGYKQFFGQK-----RRW-GARYYGFFDYNHAFIKSSFF--NSASDVWTYGFG 576

Query: 143 SDLLADIID-----KDNASFGIFGGVAIGGNTWKSSAANYWKEQIIEAKGPDVCTP 193
+D L + I+ + S G+FGG+A+ G +W +S E +
Sbjct: 577 ADALYNFINDKATNFLGKNNKLSVGLFGGIALAGTSWLNS-----EYV----- 619

Query: 194 TYCNPAPYSTNTSTVAFQVWLNFGVRANIYK-----HNGVEFGVRVPLLINKFL 243
N Y+ +T FQ N G+R N+ + +G+E GV++P + +
Sbjct: 620 NLATVNNVYNKINTANFQFLFNGLRNMN LARAKKGS DHAAQHGIELGVKIPTINTNY 679

Query: 244 SAGPNATNLYYHLKRDYSLYL 264
S L Y +R YS+YL
Sbjct: 680 SF--MGAELKY--RRLYSVYL 696

tr Q7WV93 **Adhesin-binding fucosylated histo-blood group antigen
(Fragment)**

694

AA

[BABB] [Helicobacter pylori (Campylobacter pylori)]align

Score = 82.4 bits (202), Expect = 7e-15

Identities = 76/257 (29%), Positives = 108/257 (41%), Gaps = 63/257 (24%)

Query: 27 IGTNYQLGQARLNSNIYNTGDCTGSVVGCPGLTANKHNPGGTNINWHISKYANGALNGFG 86
I TNY L N N YN +G P K G+ N NGA+NG G
Sbjct: 481 IETNYYL-----NQNSYNQIQITINQELGRNP---FRKVGIVGSQTN-----NGAMNGIG 526

Query: 87 LNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLGKQVYAPNKIQLDMSVSWGVGSDLL 146
+ VGYK+FF K KW G R YG FDY HA + + D+ ++G G+D L
Sbjct: 527 IQVGYKQFFGQK----RKW-GARYYGGFDYNHAFIKSSFF--NSASDVWTYGFGADAL 577

Query: 147 ADIID-----KDNASFGIFGGVAIGGNTWKSSAANYWKEQIIEAKGPDVCTPTYCN 197
+ I+ + S G+FGG+A+ G +W +S E +
Sbjct: 578 YNFINDKATNFLGKNNKLSVGLFGGIALAGTSLWLS-----EYV-----NLAT 620

Query: 198 PNAPYSTNTSTVAFQVWLNFGVRANIYK-----HNGVEFGVRVPLLINKFLSAGP 247
N Y+ + FQ N GVR N+ + +G+E GV++P + + S
Sbjct: 621 VNNVYNAKMNVANFQFLFNMGVRMNLARSKKKGSDHAAQHGIELGVKIPTINTNYYSF-- 678

Query: 248 NATNLYYHLKRDYSLYL 264
L Y +R YS+YL
Sbjct: 679 MGAELKY--RRLYSVYL 693

tr Q7WVA4 Adhesin-binding fucosylated histo-blood group antigen 704
(Fragment) AA
[BABB] [Helicobacter pylori (Campylobacter pylori)] align

Score = 82.4 bits (202), Expect = 7e-15

Identities = 76/257 (29%), Positives = 108/257 (41%), Gaps = 63/257 (24%)

Query: 27 IGTNYQLGQARLNSNIYNTGDCTGSVVGCPGLTANKHNPGGTNINWHISKYANGALNGFG 86
I TNY L N N YN +G P K G+ N NGA+NG G
Sbjct: 491 IETNYYL-----NQNSYNQIQITINQELGRNP---FRKVGIVGSQTN-----NGAMNGIG 536

Query: 87 LNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLGKQVYAPNKIQLDMSVSWGVGSDLL 146
+ VGYK+FF K KW G R YG FDY HA + + D+ ++G G+D L
Sbjct: 537 IQVGYKQFFGQK----RKW-GARYYGGFDYNHAFIKSSFF--NSASDVWTYGFGADAL 587

Query: 147 ADIID-----KDNASFGIFGGVAIGGNTWKSSAANYWKEQIIEAKGPDVCTPTYCN 197
+ I+ + S G+FGG+A+ G +W +S E +
Sbjct: 588 YNFINDKATNFLGKNNKLSVGLFGGIALAGTSLWLS-----EYV-----NLAT 630

Query: 198 PNAPYSTNTSTVAFQVWLNFGVRANIYK-----HNGVEFGVRVPLLINKFLSAGP 247
N Y+ + FQ N GVR N+ + +G+E GV++P + + S
Sbjct: 631 VNNVYNAKMNVANFQFLFNMGVRMNLARPKKKGSDHAAQHGIELGVKIPTINTNYYSF-- 688

Query: 248 NATNLYYHLKRDYSLYL 264
L Y +R YS+YL
Sbjct: 689 MGAELKY--RRLYSVYL 703

tr Q7WV92 Adhesin-binding fucosylated histo-blood group antigen 694

(Fragment)
[BABB] [Helicobacter pylori (Campylobacter pylori)]

AA
align

Score = 82.0 bits (201), Expect = 9e-15
Identities = 73/261 (27%), Positives = 109/261 (40%), Gaps = 71/261 (27%)

Query: 27 IGTNYQLGQARLNSNIYNTGDCTGSVVGCPP----GLTANKHNPGGTNINWHSKYANGAL 82
I TNY L N N YN +G P G+ +++ N NGA+
Sbjct: 481 IETNYYL-----NQNSYNQIQITINQELGRNPFRKVGIVSSQTN-----NGAM 522

Query: 83 NGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLGKQVYAPNKIQLDMVSWG VG 142
NG G+ VGYK+FF K +W G R YG FDY HA + + D+ ++G G
Sbjct: 523 NGIGIQVGYKQFFGQK----RRW-GARYYGFFDYNHAFIKSSFF--NSASDVWTYGFG 573

Query: 143 SDLLADIID-----KDNASFGIFGGVAIGGNTWKSSAANYWKEQIIIEAKGPDVCTP 193
+D L + I+ + S G+FGG+A+ G +W +S
Sbjct: 574 ADALYNFINDKATNFLGKNNKLSVGLFGGIALAGTSWLNSE-----FV 616

Query: 194 TYCNP NAPYSTNTSTVAFQVWLNFGVRANIYK-----HNGVEFGVRVPLLINKFL 243
N Y+ +T FQ N G+R N+ + +G+E GV++P + +
Sbjct: 617 NLATVNNVYNAKINTANFQFLFNLGLRMNLARAKKKGSDHAAQHGIELGVKIPTINTNY 676

Query: 244 SAGPNATNLYYHLKRDYSLYL 264
S L Y +R YS+YL
Sbjct: 677 SF--MGAELKY--RRLYSVYL 693

tr Q7WV99 Adhesin-binding fucosylated histo-blood group antigen
(Fragment)
[BABB] [Helicobacter pylori (Campylobacter pylori)]

694
AA
align

Score = 82.0 bits (201), Expect = 9e-15
Identities = 74/261 (28%), Positives = 110/261 (41%), Gaps = 71/261 (27%)

Query: 27 IGTNYQLGQARLNSNIYNTGDCTGSVVGCPP----GLTANKHNPGGTNINWHSKYANGAL 82
I TNY L N N YN +G P G+ +++ N NGA+
Sbjct: 481 IETNYYL-----NQNAYNQIQITINQELGRNPFRKVGIVSSQTN-----NGAM 522

Query: 83 NGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLGKQVYAPNKIQLDMVSWG VG 142
NG G+ VGYK+FF K KW G R YG FDY HA + + D+ ++G G
Sbjct: 523 NGIGIQVGYKQFFGQK----RKW-GARYYGFFDYNHAFIKSSFF--NSASDVWTYGFG 573

Query: 143 SDLLADIID-----KDNASFGIFGGVAIGGNTWKSSAANYWKEQIIIEAKGPDVCTP 193
+D L + I+ + S G+FGG+A+ G +W +S E +
Sbjct: 574 ADALYNFINDKATNFLGKNNKLSVGLFGGIALAGTSWLNS-----EYV----- 616

Query: 194 TYCNP NAPYSTNTSTVAFQVWLNFGVRANIYK-----HNGVEFGVRVPLLINKFL 243
N Y+ + FQ N GVR N+ + +G+E G+++P + +
Sbjct: 617 NLATVNNVYNAKMNVANFQFLFNMGVRMNLARSKKKGSDHAAQHGIELGLKIPTINTNY 676

Query: 244 SAGPNATNLYYHLKRDYSLYL 264
S L Y +R YS+YL
Sbjct: 677 SF--MGAELKY--RRLYSVYL 693

tr Q7WVA0 **Adhesin-binding fucosylated histo-blood group antigen** 696
(Fragment) AA
[BABB] [*Helicobacter pylori* (*Campylobacter pylori*)] align

Score = 82.0 bits (201), Expect = 9e-15
Identities = 74/261 (28%), Positives = 110/261 (41%), Gaps = 71/261 (27%)

Query: 27 IGTNYQLGQARLNSNIYNTGDCTGSVVGCPP----GLTANKHNPGGTNINWHSKYANGAL 82
I TNY L N N YN +G P G+ +++ N NGA+
Sbjct: 483 IETNYYL-----NQNTYNQIQITINQELGRNPFRKVGIVSSQTN-----NGAM 524

Query: 83 NGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLGKQVYAPNKIQLDMVSWGVG 142
NG G+ VGYK+FF K KW G R YG FDY HA + + D+ ++G G
Sbjct: 525 NGIGIQVGYKQFFGQK-----RKW-GARYYGFFDYNHAFIKSSFF--NSASDVWTYGF 575

Query: 143 SDLLADIID-----KDNASFGIFGGVAIGGNTWKSSAANYWKEQIIEAKGPDVCTP 193
+D L + I+ + S G+FGG+A+ G +W +S E +
Sbjct: 576 ADALYNFINDKATNFLGKNNKLSVGLFGGIALAGTSWLNS-----EYV----- 618

Query: 194 TYCNP NAPYSTNTSTVAFQVWLNFGVRANIYK-----HNGVEFGVRVPLLINKFL 243
N Y+ + FQ N GVR N+ + +G+E G+++P + +
Sbjct: 619 NLATVNNVYNAKMNVANFQFLFNMGVRMNLARSKKKGSDHAAQHGIELGLKIPTINTNYY 678

Query: 244 SAGPNATNLYYHLKRDYSLYL 264
S L Y +R YS+YL
Sbjct: 679 SF--MGAELKY--RRLYSVYL 695

tr Q7WVA2 **Adhesin-binding fucosylated histo-blood group antigen** 695
(Fragment) AA
[BABB] [*Helicobacter pylori* (*Campylobacter pylori*)] align

Score = 82.0 bits (201), Expect = 9e-15
Identities = 74/261 (28%), Positives = 110/261 (41%), Gaps = 71/261 (27%)

Query: 27 IGTNYQLGQARLNSNIYNTGDCTGSVVGCPP----GLTANKHNPGGTNINWHSKYANGAL 82
I TNY L N N YN +G P G+ +++ N NGA+
Sbjct: 482 IDTNYYL-----NQNSYNQIQITINQELGRNPFRKVGIVSSQTN-----NGAM 523

Query: 83 NGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLGKQVYAPNKIQLDMVSWGVG 142
NG G+ VGYK+FF K KW G R YG FDY HA + + D+ ++G G
Sbjct: 524 NGIGIQVGYKQFFGQK-----RKW-GARYYGFFDYNHAFIKSSFF--NSASDVWTYGF 574

Query: 143 SDLLADIID-----KDNASFGIFGGVAIGGNTWKSSAANYWKEQIIEAKGPDVCTP 193
+D L + I+ + S G+FGG+A+ G +W +S E +
Sbjct: 575 ADALYNFINDKATNFLGKNNKLSVGLFGGIALAGTSWLNS-----EYV----- 617

Query: 194 TYCNP NAPYSTNTSTVAFQVWLNFGVRANIYK-----HNGVEFGVRVPLLINKFL 243
N Y+ + FQ N GVR N+ + +G+E G+++P + +
Sbjct: 618 NLATMNNVYNAKMNVANFQFLFNMGVRMNLARPKKKSDHAAQHGIELGLKIPTINTNYY 677

Query: 244 SAGPNATNLYYHLKRDYSLYL 264
S L Y +R YS+YL
Sbjct: 678 SF--MGAELKY--RRLYSVYL 694

Score = 81.6 bits (200), Expect = 1e-14

Identities = 73/260 (28%), Positives = 108/260 (41%), Gaps = 71/260 (27%)

```
Query: 27  IGTNYQLGQARLNSNIYNTGDCTGSVVGCPP----GLTANKHNPGGTNINWHSKYANGAL 82
          I TNY L      N N YN      +G P      G+ +++ N      NGA+
Sbjct: 527 IETNYYL-----NQNSYNQIQITINQELGRNPFRKMGIVSSQTN-----NGAM 568

Query: 83  NGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLGKQVYAPNKIQLDMVSWGVG 142
          NG G+ VGYK+FF K      +W G R YG FDY HA +      +      D+ ++G G
Sbjct: 569 NGIGIQVGYKQFFGQK-----RRW-GARYYGFFDYNHAFIKSSFF---NSASDVWTYGFG 619

Query: 143 SDLLADIID-----KDNASFGIFGGVAIGGNTWKSSAANYWKEQIIEAKGPDVCTP 193
          +D L + I+      + S G+FGG+A+ G +W +S
Sbjct: 620 ADALYNFINDKATNFLGKNNKLSVGLFGGIALAGTSWLNSE-----FV 662

Query: 194 TYCNP NAPYSTNTSTVAFQVWLNFGVRANIYK-----HNGVEFGVRVPLLINKFL 243
          N Y+   +T FQ   N GVR N+ +      +G+E GV++P +   +
Sbjct: 663 NLATVNNVYNAKINTANFQFLFNMGVRMNLARAKKKGSDHAAQHGIELGVKIPTINTNYY 722

Query: 244 SAGPNATNLYYHLKRDYSLY 263
          S      L Y   +R YS+Y
Sbjct: 723 SF--MGAELKY--RRLYSVY 738
```

tr Q7WV87 **Adhesin-binding fucosylated histo-blood group antigen** 694
(Fragment) AA
[BABB] [*Helicobacter pylori* (*Campylobacter pylori*)] align

Score = 81.6 bits (200), Expect = 1e-14

Identities = 73/261 (27%), Positives = 109/261 (40%), Gaps = 71/261 (27%)

```
Query: 27  IGTNYQLGQARLNSNIYNTGDCTGSVVGCPP----GLTANKHNPGGTNINWHSKYANGAL 82
          I TNY L      N N YN      +G P      G+ +++ N      NGA+
Sbjct: 481 IETNYYL-----NPNSYNQIQITINQELGRNPFRKMGIVSSQTN-----NGAM 522

Query: 83  NGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLGKQVYAPNKIQLDMVSWGVG 142
          NG G+ VGYK+FF K      +W G R YG FDY HA +      +      D+ ++G G
Sbjct: 523 NGIGIQVGYKQFFGQK-----RRW-GARYYGFFDYNHAFIKSSFF---NSASDVWTYGFG 573

Query: 143 SDLLADIID-----KDNASFGIFGGVAIGGNTWKSSAANYWKEQIIEAKGPDVCTP 193
          +D L + I+      + S G+FGG+A+ G +W +S
Sbjct: 574 ADALYNFINDKATNFLGKNNKLSVGLFGGIALAGTSWLNSE-----FV 616

Query: 194 TYCNP NAPYSTNTSTVAFQVWLNFGVRANIYK-----HNGVEFGVRVPLLINKFL 243
          N Y+   +T FQ   N G+R N+ +      +G+E GV++P +   +
Sbjct: 617 NLATVNNVYNAKINTANFQFLFNLGLRMNLARAKKKGNDHAAQHGIELGVKIPTINTNYY 676

Query: 244 SAGPNATNLYYHLKRDYSLYL 264
          S      L Y   +R YS+YL
Sbjct: 677 SF--MGAELKY--RRLYSVYL 693
```

tr Q7WV98 **Adhesin-binding fucosylated histo-blood group antigen** 694
(Fragment) AA
[BABB] [*Helicobacter pylori* (*Campylobacter pylori*)] align

Score = 81.6 bits (200), Expect = 1e-14

Identities = 74/261 (28%), Positives = 110/261 (41%), Gaps = 71/261 (27%)

Query: 27 IGTNYQLGQARLNSNIYNTGDCTGSVVGCPP----GLTANKHNPGGTNINWHSKYANGAL 82
I TNY L N N YN +G P G+ +++ N NGA+
Sbjct: 481 IETNYYL-----NQNSYNQIQITINQELGRNPFRKVG MVSSQTN-----NGAM 522

Query: 83 NGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLGKQVYAPNKIQLDMVSWG VG 142
NG G+ VGYK+FF K KW G R YG FDY HA + + D+ ++G G
Sbjct: 523 NGIGIQVGYKQFFGQK-----RKW-GARYYGFFDYNHAFIKSSFF--NSASDVW TYGFG 573

Query: 143 SDLLADIID-----KDNASFGIFGGVAIGGNTWKSSAANYWKEQIIEAKGPDVCTP 193
+D L + I+ + S G+FGG+A+ G +W +S E +
Sbjct: 574 ADALYNFINDKATNFLGKNNKLSVGLFGGIALAGTSWLNS-----EYV----- 616

Query: 194 TYCNP NAPYSTNTSTVAFQVWLNFGVRANIYK-----HNGVEFGVRVPLLINKFL 243
N Y+ + FQ N GVR N+ + +G+E G+++P + +
Sbjct: 617 NLATVNNVYNAKLVANFQFLFNMGVRMNLARSKKKGSDHVAQHGIELGLKIPTINTNYY 676

Query: 244 SAGPNATNLYYHLKRDYSLYL 264
S L Y +R YS+YL
Sbjct: 677 SF--MGAELKY--RRLYSVYL 693

tr Q7WVA1 **Adhesin-binding fucosylated histo-blood group antigen** 695
(Fragment) AA
[BABB] [*Helicobacter pylori* (*Campylobacter pylori*)] align

Score = 81.6 bits (200), Expect = 1e-14

Identities = 74/261 (28%), Positives = 110/261 (41%), Gaps = 71/261 (27%)

Query: 27 IGTNYQLGQARLNSNIYNTGDCTGSVVGCPP----GLTANKHNPGGTNINWHSKYANGAL 82
I TNY L N N YN +G P G+ +++ N NGA+
Sbjct: 482 IETNYYL-----NQNSYNQIQITINQELGRNPFRKVGIVSSQTN-----NGAM 523

Query: 83 NGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLGKQVYAPNKIQLDMVSWG VG 142
NG G+ VGYK+FF K KW G R YG FDY HA + + D+ ++G G
Sbjct: 524 NGIGIQVGYKQFFGQK-----RKW-GARYYGFFDYNHAFIKSSFF--NSASDVW TYGFG 574

Query: 143 SDLLADIID-----KDNASFGIFGGVAIGGNTWKSSAANYWKEQIIEAKGPDVCTP 193
+D L + I+ + S G+FGG+A+ G +W +S E +
Sbjct: 575 ADALYNFINDKATNFLGKNNKLSVGLFGGIALAGTSWLNS-----EYV----- 617

Query: 194 TYCNP NAPYSTNTSTVAFQVWLNFGVRANIYK-----HNGVEFGVRVPLLINKFL 243
N Y+ + FQ N GVR N+ + +G+E G+++P + +
Sbjct: 618 NLATMNNVYNAKMNVANFQFLFNMGVRMNLARPKKKGSDHAAQHGIELGLKIPTINTNYY 677

Query: 244 SAGPNATNLYYHLKRDYSLYL 264
S L Y +R YS+YL
Sbjct: 678 SF--MGAELKY--RRLYSVYL 694

Score = 81.3 bits (199), Expect = 1e-14

Identities = 72/262 (27%), Positives = 113/262 (42%), Gaps = 55/262 (20%)

```

Query: 24  GVIIGTNYQLGQARLNSNIYNTGDCTGSVVGCPGLTANKHNPGGTNINWHSKYANG--- 80
          G  +      + QAR      + NT +      V      L AN      W  +A G
Sbjct: 308  GYQVSYGGHIDQARSTQLLNNTTNTLAKVTALNNELKANP-----WLGNFAGNSS 358

Query: 81  ---ALNGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLGKQVYAPNKIQLDMV 137
          A NGF  +GYK+FF      +K  G R YG F Y  A +G      P  Q++++
Sbjct: 359  QVNAFNGFITKIGYKQFFG-----ENKNVGLRYYGFFSYNGAGVGN---GPTYNQVNLL 409

Query: 138  SWGVGSDLLADIIDKD---NASFGIFGGVAIGGNTWKSSAANYWKEQIIIEAKGPDVCTP 193
          ++GVG+D+L ++  +      + + G FGG+ + G+T+ S+  N      P  +
Sbjct: 410  TYGVGTDVLYNVFSRSFSGSRSLNAGFFGGIQLAGDTYISTLRN-----SPQLA-- 457

Query: 194  TYCNPAPYSTNTSTVAFQVWL--NFGV-RANIYKHN--GVEFGVRVPLLINKFLSAGPN 248
          N P +T      + F V L  NFG+ + ++  HN  +E GV++P + N +  AG
Sbjct: 458  -----NRPTATKFQFL-FDVGLRMNFGILKKDLKSHNQHSIEIGVQIPTIYNTYYKAGGA 511

Query: 249  ATNLYYHLKRDYSLYLGYN YTF 270
          +      R YS+Y  Y Y F
Sbjct: 512  EVKYF----RPYSVYWVYGYAF 529

```

```

tr  Q7WV67  Adhesin-binding fucosylated histo-blood group antigen      734
          (Fragment)                                                    AA
          [BABB] [Helicobacter pylori (Campylobacter pylori)]          align

```

Score = 81.3 bits (199), Expect = 1e-14

Identities = 74/260 (28%), Positives = 109/260 (41%), Gaps = 71/260 (27%)

```

Query: 27  IGTNYQLGQARLNSNIYNTGDCTGSVVGCP-----GLTANKHNPGGTNINWHSKYANGAL 82
          I TNY L      N N YN      +G  P      G+ +++ N      NGA+
Sbjct: 523  IETNYYL-----NQNSYNQIQTINQELGRNPFRKVGIVSSQTN-----NGAM 564

Query: 83  NGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLGKQVYAPNKIQLDMVSWGVG 142
          NG G+ VGYK+FF  K      KW G R YG FDY HA +      +      D+ ++G G
Sbjct: 565  NGIGIQVGYKQFFGQK-----RKW-GARYYGFFDYNHAFIKSSFF---NSASDVWTYGFG 615

Query: 143  SDLLADIID-----KDNASFGIFGGVAIGGNTWKSSAANYWKEQIIIEAKGPDVCTP 193
          +D L + I+      +  S G+FGG+A+ G +W +S      E  +
Sbjct: 616  ADALYNFINDKATNFLGKNNKLSVGLFGGIALAGTSWLNS-----EYV----- 658

Query: 194  TYCNPAPYSTNTSTVAFQVWLNFGVRANIYK-----HNGVEFGVRVPLLINKFL 243
          N  Y+  +  FQ  N GVR N+ +      +G+E GV++P +  +
Sbjct: 659  NLATVNNVYNAKMNVANFQFLFMGMVRMNLARSKKKGSDHAAQHGIELGVKIPTINTNY 718

Query: 244  SAGPNATNLYYHLKRDYSLY 263
          S      L Y  +R YS+Y
Sbjct: 719  SF--MGAELKY--RRLYSVY 734

```

tr Q7WV69 **Adhesin-binding fucosylated histo-blood group antigen** 736
(Fragment) AA
[BABB] [*Helicobacter pylori* (*Campylobacter pylori*)] align

Score = 81.3 bits (199), Expect = 1e-14
Identities = 75/256 (29%), Positives = 107/256 (41%), Gaps = 63/256 (24%)

Query: 27 IGTNYQLGQARLNSNIYNTGDCTGSVVGCPPGLTANKHNPGGTNINWHSKYANGALNGFG 86
I TNY L N N YN +G P K G+ N NGA+NG G
Sbjct: 525 IETNYYL-----NQNSYNQVQTINQELGRNP---FRKVGIVGSQTN-----NGAMNGIG 570

Query: 87 LNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLGKQVYAPNKIQLDMVSWGVSDDL 146
+ VGYK+FF K KW G R YG FDY HA + + D+ ++G G+D L
Sbjct: 571 IQVGYKQFFGQK-----RKW-GARYYGFFDYNHAFIKSSFF---NSASDVWTYGFADAL 621

Query: 147 ADIID-----KDNASFGIFGGVAIGGNTWKSSAANYWKEQIIIEAKGPDVCTPTYCN 197
+ I+ + S G+FGG+A+ G +W +S E +
Sbjct: 622 YNFINDKATNFLGKNNKLSVGLFGGIALAGTSWLNS-----EYV-----NLAT 664

Query: 198 PNAPYSTNTSTVAFQVWLNFGVRANIYK-----HNGVEFGVRVPLLINKFLSAGP 247
N Y+ + FQ N GVR N+ + +G+E GV++P + + S
Sbjct: 665 VNNVYNAKMNVANFQFLFNMGVRMNLARAKKKGSDHAAQHGIELGVKIPTINTNYYSF-- 722

Query: 248 NATNLYYHLKRDYSLY 263
L Y +R YS+Y
Sbjct: 723 MGAELKY--RRLYSVY 736

tr Q7WV71 **Adhesin-binding fucosylated histo-blood group antigen** 734
(Fragment) AA
[BABB] [*Helicobacter pylori* (*Campylobacter pylori*)] align

Score = 81.3 bits (199), Expect = 1e-14
Identities = 73/260 (28%), Positives = 110/260 (42%), Gaps = 71/260 (27%)

Query: 27 IGTNYQLGQARLNSNIYNTGDCTGSVVGCPP---GLTANKHNPGGTNINWHSKYANGAL 82
I TNY L N N YN +G P G+ +++ N NGA+
Sbjct: 523 IETNYYL-----NQNSYNQVQTINQELGRNPFRKMGISSQTN-----NGAM 564

Query: 83 NGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLGKQVYAPNKIQLDMVSWGVS 142
NG G+ VGYK+FF K +W G R YG FDY HA + + D+ ++G G
Sbjct: 565 NGIGIQVGYKQFFGQK-----RRW-GARYYGFFDYNHAFIKSNFF---NSASDVWTYGF 615

Query: 143 SDLLADIID-----KDNASFGIFGGVAIGGNTWKSSAANYWKEQIIIEAKGPDVCTP 193
+D L + I+ + S G+FGG+A+ G +W +S E +
Sbjct: 616 ADALYNFINDKATNFLGKNNKLSVGLFGGIALAGTSWLNS-----EYV----- 658

Query: 194 TYCNPAPYSTNTSTVAFQVWLNFGVRANIYK-----HNGVEFGVRVPLLINKFL 243
N Y+ +T FQ N G+R N+ + +G+E GV++P + +
Sbjct: 659 NLATVNNVYNAKINTANFQFLFNLGLRMNLARAKKKGSDHAAQHGIELGVKIPTINTNYY 718

Query: 244 SAGPNATNLYYHLKRDYSLY 263
S L Y +R YS+Y
Sbjct: 719 SF--MGAELKY--RRLYSVY 734

Score = 81.3 bits (199), Expect = 1e-14

Identities = 75/256 (29%), Positives = 107/256 (41%), Gaps = 63/256 (24%)

```

Query: 27  IGTNYQLGQARLNSNIYNTGDC TGSVVGCPPGLTANKHNPGGTNINWHSKYANGALNGFG 86
          I TNY L      N N YN      +G P      K      G+ N      NGA+NG G
Sbjct: 526 IDTNYYL-----NQNSYNQIQ TINQELGRNP---FRKVGIVGSQTN-----NGAMNGIG 571

Query: 87  LNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLGKQVYAPNKIQLDMVSWGVSDDL 146
          + VGYK+FF K      KW G R YG FDY HA +      +      D+ ++G G+D L
Sbjct: 572 IQVGYKQFFGQK-----RKW-GARYYGFFDYNHAFIKSSFF---NSASDVWTYGF GADAL 622

Query: 147 ADIID-----KDNASFGIFGGVAIGGNTWKSSAANYWKEQIIIEAKGPDVCTPTYCN 197
          + I+      + S G+FGG+A+ G +W +S      E +
Sbjct: 623 YNFINDKATNFLGKNNKLSVGLFGGIALAGTSWLNS-----EYV-----NLAT 665

Query: 198 PNAPYSTNTSTVAFQVWLNFGVRANIYK-----HNGVEFGVRVPLLINKFLSAGP 247
          N Y+      + FQ      N GVR N+ +      +G+E GV++P +      + S
Sbjct: 666 VNNVYNAKMNVANFQFLFNMGVRMNLARSKKKGSDHAAQHGIELGVKIPTINTNYYSF-- 723

Query: 248 NATNLYYHLKRDYSLY 263
          L Y      +R YS+Y
Sbjct: 724 MGAELKY--RRLYSVY 737

```

```

tr Q7WV88 Adhesin-binding fucosylated histo-blood group antigen 696
          (Fragment) AA
          [BABB] [Helicobacter pylori (Campylobacter pylori)] align

```

Score = 81.3 bits (199), Expect = 1e-14

Identities = 73/261 (27%), Positives = 108/261 (40%), Gaps = 71/261 (27%)

```

Query: 27  IGTNYQLGQARLNSNIYNTGDC TGSVVGCPP----GLTANKHNPGGTNINWHSKYANGAL 82
          I TNY L      N N YN      +G P      G+ +++ N      NGA+
Sbjct: 483 IETNYYL-----NQNSYNQIQ TINQELGRNPFRKMGIVSSQTN-----NGAM 524

Query: 83  NGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLGKQVYAPNKIQLDMVSWGVS 142
          NG G+ VGYK+FF K      +W G R YG FDY HA +      +      D+ ++G G
Sbjct: 525 NGIGIQVGYKQFFGQK-----RRW-GARYYGFFDYNHAFIKSSFF---NSASDVWTYGF 575

Query: 143 SDLLADIID-----KDNASFGIFGGVAIGGNTWKSSAANYWKEQIIIEAKGPDVCTP 193
          +D L + I+      + S G+FGG+A+ G +W +S
Sbjct: 576 ADALYNFINDKATNFLGKNNKLSVGLFGGIALAGTSWLNSE-----FV 618

Query: 194 TYCNPAPYSTNTSTVAFQVWLNFGVRANIYK-----HNGVEFGVRVPLLINKFL 243
          N Y+      + FQ      N GVR N+ +      +G+E GV++P +      +
Sbjct: 619 NLATVNNVYNAKMNVANFQFLFNMGVRMNLARAKKKGSDHAAQHGIELGVKIPTINTNYY 678

Query: 244 SAGPNATNLYYHLKRDYSLYL 264
          S      L Y      +R YS+YL
Sbjct: 679 SF--MGAELKY--RRLYSVYL 695

```

tr Q7WV68 **Adhesin-binding fucosylated histo-blood group antigen** 733
 (Fragment) AA
 [BABB] [*Helicobacter pylori* (*Campylobacter pylori*)] align

Score = 80.9 bits (198), Expect = 2e-14
 Identities = 75/256 (29%), Positives = 107/256 (41%), Gaps = 63/256 (24%)

Query: 27 IGTNYQLGQARLNSNIYNTGDCTGSVVGCPPGLTANKHNPGGTNINWHSKYANGALNGFG 86
 I TNY L N N YN +G P K G+ N NGA+NG G
 Sbjct: 522 IETNYYL-----NQNSYNQIQITINQELGRNP---FRKVGIVGSQTN-----NGAMNGIG 567

Query: 87 LNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLGKQVYAPNKIQLDMVSWGVSDDL 146
 + VGYK+FF K KW G R YG FDY HA + + D+ ++G G+D L
 Sbjct: 568 IQVGYKQFFGQK-----RKW-GARYYGFFDYNHAFIKSSFF---NSASDVWITYGFGADAL 618

Query: 147 ADIID-----KDNASFGIFGGVAIGGNTWKSSAANYWKEQIIEAKGPDVCTPTYCN 197
 + I+ + S G+FGG+A+ G +W +S E +
 Sbjct: 619 YNFINDKATNFLGKNNKLSVGLFGGIALAGTSWLNS-----EYV-----NLAT 661

Query: 198 PNAPYSTNTSTVAFQVWLNFGVRANIYK-----HNGVEFGVRVPLLINKFLSAGP 247
 N Y+ + FQ N GVR N+ + +G+E GV++P + + S
 Sbjct: 662 VNNVYNAKMNVANFQFLFNMGVRMNLARSKKKGSDHAAQHGIELGVKIPTINTNYYSF-- 719

Query: 248 NATNLYYHLKRDYSLY 263
 L Y +R YS+Y
 Sbjct: 720 MGAELKY--RRLYSVY 733

tr Q7WV77 **Adhesin-binding fucosylated histo-blood group antigen** 734
 (Fragment) AA
 [BABB] [*Helicobacter pylori* (*Campylobacter pylori*)] align

Score = 80.9 bits (198), Expect = 2e-14
 Identities = 72/261 (27%), Positives = 108/261 (40%), Gaps = 73/261 (27%)

Query: 27 IGTNYQLGQARLNSNIYNTGDCTGSVVGCPP----GLTANKHNPGGTNINWHSKYANGAL 82
 I TNY L N N YN +G P G+ +++ N NGA+
 Sbjct: 523 IETNYYL-----NQNSYNQIQITINQELGRNPFRKVGIVSSQTN-----NGAM 564

Query: 83 NGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDYGHADLGKQVYAPNKIQLDMVSWGVS 142
 NG G+ VGYK+FF K +W G R YG FDY HA + + D+ ++G G
 Sbjct: 565 NGIGIQVGYKQFFGQK-----RRW-GARYYGFFDYNHAFIKSSFF---NSASDVWITYGFG 615

Query: 143 SDLLADIID-----KDNASFGIFGGVAIGGNTWKSSAANYWKEQIIEAKGPDVCTP 193
 +D L + I+ + S G+FGG+A+ G +W +S
 Sbjct: 616 ADALYNFINDKATNFLGKNNKLSVGLFGGIALAGTSWLNSE-----FV 658

Query: 194 TYCNPAPYSTNTSTVAFQVWLNFGVRANIYK-----HNGVEFGVRVPLLINKFL 243
 N Y+ +T FQ N G+R N+ + +G+E GV++P + +
 Sbjct: 659 NLATVNNVYNAKINTANFQFLFNLGLRMNLARAKKKGSDHAAQHGIELGVKIPTINTNY 718

Query: 244 S-AGPNATNLYYHLKRDYSLY 263
 S G N +R YS+Y
 Sbjct: 719 SFGAELKN-----RRLYSVY 734

Database: EXPASY/UniProt

Posted date: Apr 25, 2004 4:51 AM

Number of letters in database: 465,400,423

Number of sequences in database: 1,459,789

Lambda	K	H
0.319	0.139	0.446

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

length of query: 270

length of database: 465,400,423

effective HSP length: 122

effective length of query: 148

effective length of database: 287,306,165

effective search space: 42521312420

effective search space used: 42521312420

T: 11

A: 40

X1: 16 (7.4 bits)

X2: 38 (14.6 bits)

X3: 64 (24.7 bits)

S1: 41 (21.7 bits)

S2: 72 (32.3 bits)

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<input type="checkbox"/> tr Q8GDJ2	HopQ [HOPQ] [Helicobacter pylori (Campylobacter pylori)]	98	2e-19
<input type="checkbox"/> tr Q8GDJ3	HopQ [HOPQ] [Helicobacter pylori (Campylobacter pylori)]	98	2e-19
<input type="checkbox"/> tr Q9X745	HopZ protein precursor [HOPZ] [Helicobacter pylori (Ca...]	97	3e-19
<input type="checkbox"/> tr Q25015	Outer membrane protein (OMP6) [HP0229] [Helicobacter p...]	97	3e-19
<input type="checkbox"/> tr Q8GDI8	HopQ [HOPQ] [Helicobacter pylori (Campylobacter pylori)]	97	3e-19
<input type="checkbox"/> tr Q8GDJ1	HopQ [HOPQ] [Helicobacter pylori (Campylobacter pylori)]	97	3e-19
<input type="checkbox"/> tr Q8GDJ4	HopQ [HOPQ] [Helicobacter pylori (Campylobacter pylori)]	97	3e-19
<input type="checkbox"/> tr Q9ZK39	Putative outer membrane function [JHP1103] [Helicobact...]	96	6e-19
<input type="checkbox"/> tr Q9ZMK5	Outer membrane protein/porin [HOPA] [Helicobacter pylo...]	96	6e-19
<input type="checkbox"/> tr Q25791	Outer membrane protein (OMP27) [HP1177] [Helicobacter ...]	96	6e-19
<input type="checkbox"/> tr Q8GDJ0	HopQ [HOPQ] [Helicobacter pylori (Campylobacter pylori)]	96	6e-19
<input type="checkbox"/> tr Q9X747	HopZ protein precursor [HOPZ] [Helicobacter pylori (Ca...]	96	6e-19
<input type="checkbox"/> tr Q9ZN51	Putative outer membrane protein [JHP0007] [Helicobacte...]	96	8e-19
<input type="checkbox"/> tr Q9X746	HopZ protein precursor [HOPZ] [Helicobacter pylori (Ca...]	96	8e-19
<input type="checkbox"/> tr Q9X748	HopZ protein precursor [HOPZ] [Helicobacter pylori (Ca...]	96	8e-19
<input type="checkbox"/> tr Q8GDI6	HopQ [HOPQ] [Helicobacter pylori (Campylobacter pylori)]	95	1e-18
<input type="checkbox"/> tr Q8GDI7	HopQ [HOPQ] [Helicobacter pylori (Campylobacter pylori)]	95	1e-18
<input type="checkbox"/> tr Q9ZMV0	Putative outer membrane protein [JHP0117] [Helicobacte...]	95	1e-18
<input type="checkbox"/> tr Q24941	Hypothetical protein HP0127 [HP0127] [Helicobacter pyl...]	95	1e-18
<input type="checkbox"/> tr Q9ZKS8	Putative outer membrane protein [JHP0857] [Helicobacte...]	94	3e-18
<input type="checkbox"/> tr Q9ZLZ6	Putative outer membrane protein [JHP0429] [Helicobacte...]	94	3e-18
<input type="checkbox"/> tr Q8GDI9	HopQ [HOPQ] [Helicobacter pylori (Campylobacter pylori)]	94	3e-18
<input type="checkbox"/> tr Q9S3I7	HopZ protein precursor [HOPZ] [Helicobacter pylori (Ca...]	93	4e-18
<input type="checkbox"/> tr Q9ZLB8	Putative outer membrane protein [JHP0662] [Helicobacte...]	93	5e-18
<input type="checkbox"/> tr Q9ZLC1	Putative outer membrane protein [JHP0659] [Helicobacte...]	93	5e-18
<input type="checkbox"/> tr Q9ZJ82	Putative outer membrane protein [JHP1432] [Helicobacte...]	92	6e-18
<input type="checkbox"/> tr Q9ZN38	Putative outer membrane protein [JHP0021] [Helicobacte...]	92	8e-18
<input type="checkbox"/> tr Q25945	Hypothetical protein HP1395 [HP1395] [Helicobacter pyl...]	92	1e-17
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<input type="checkbox"/> tr Q25222	Hypothetical protein HP0477 [HP0477] [Helicobacter pyl...]	92	1e-17
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<input type="checkbox"/> tr Q93HU1	HPomp29(SS1) protein [HPOMP29(SS1)] [Helicobacter pylo...]	90	3e-17
<input type="checkbox"/> tr Q93HU0	OMU116 protein [OMU116] [Helicobacter pylori (Campylob...]	89	7e-17
<input type="checkbox"/> tr Q9ZMI2	Putative outer membrane protein [JHP0238] [Helicobacte...]	89	9e-17
<input type="checkbox"/> tr Q24908	Hypothetical protein HP0079 [HP0079] [Helicobacter pyl...]	89	9e-17
<input type="checkbox"/> tr Q93HU2	HPomp29(43504) protein [HPOMP29(43504)] [Helicobacter ...]	89	9e-17
<input type="checkbox"/> tr Q25091	Hypothetical protein HP0324 [HP0324] [Helicobacter pyl...]	88	1e-16
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<input type="checkbox"/> tr Q25772	Hypothetical protein HP1157 [HP1157] [Helicobacter pyl...]	87	2e-16
<input type="checkbox"/> tr Q9X751	HopX protein precursor [HOPX] [Helicobacter pylori (Ca...]	87	2e-16
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<input type="checkbox"/> tr Q25036	Outer membrane protein (OMP8) [HP0254] [Helicobacter p...]	87	3e-16
<input type="checkbox"/> tr Q9X749	HopV protein precursor (27 kDa outer membrane protein)...	87	3e-16
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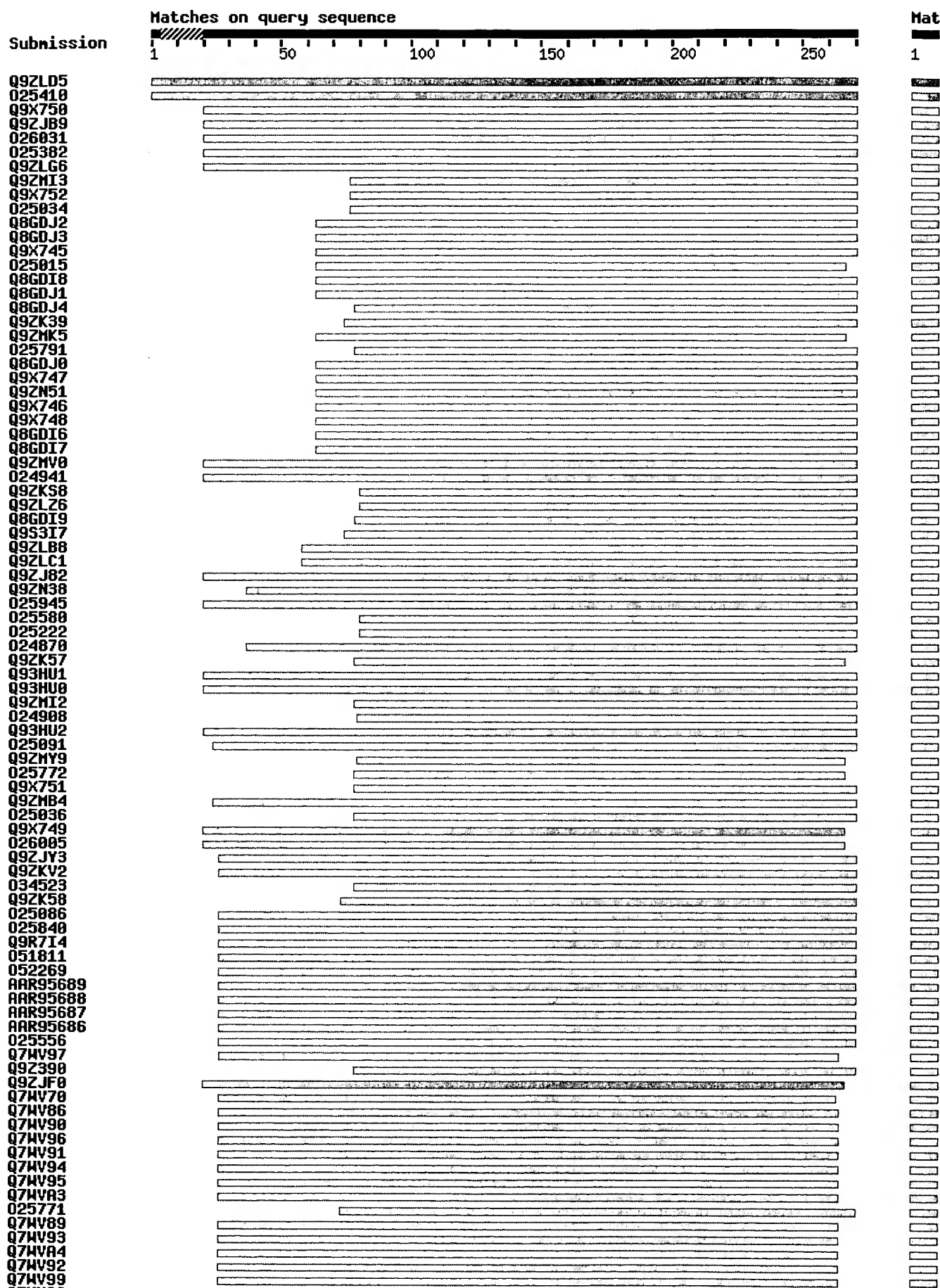
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<input type="checkbox"/>	tr Q9ZKV2	Outer membrane protein-adhesin [BABA] [Helicobacter py...	86	6e-16
<input type="checkbox"/>	tr Q34523	Hypothetical protein HP1342 [HP1342] [Helicobacter pyl...	86	6e-16
<input type="checkbox"/>	tr Q9ZK58	Putative outer membrane protein [JHP1083] [Helicobacte...	86	8e-16
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<input type="checkbox"/>	tr Q9R7I4	Adhesin-binding fucosylated histo-blood group antigen ...	86	8e-16
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<input type="checkbox"/>	tn AAR95687	BabB [Helicobacter pylori (Campylobacter pylori)]	86	8e-16
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<input type="checkbox"/>	tr Q25556	Outer membrane protein (OMP19) [HP0896] [Helicobacter ...	85	1e-15
<input type="checkbox"/>	tr Q7WV97	Adhesin-binding fucosylated histo-blood group antigen ...	84	2e-15
<input type="checkbox"/>	tr Q9Z390	Putative outer membrane protein [JHP0212] [Helicobacte...	83	4e-15
<input type="checkbox"/>	tr Q9ZJF0	Putative outer membrane protein [JHP1362] [Helicobacte...	83	4e-15
<input type="checkbox"/>	tr Q7WV70	Adhesin-binding fucosylated histo-blood group antigen ...	83	4e-15
<input type="checkbox"/>	tr Q7WV86	Adhesin-binding fucosylated histo-blood group antigen ...	83	4e-15
<input type="checkbox"/>	tr Q7WV90	Adhesin-binding fucosylated histo-blood group antigen ...	83	4e-15
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<input type="checkbox"/>	tr Q7WVA3	Adhesin-binding fucosylated histo-blood group antigen ...	83	5e-15
<input type="checkbox"/>	tr Q25771	Hypothetical protein HP1156 [HP1156] [Helicobacter pyl...	82	7e-15
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<input type="checkbox"/>	tr Q7WVA2	Adhesin-binding fucosylated histo-blood group antigen ...	82	9e-15
<input type="checkbox"/>	tr Q7WV75	Adhesin-binding fucosylated histo-blood group antigen ...	82	1e-14
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<input type="checkbox"/>	tr Q7WVA1	Adhesin-binding fucosylated histo-blood group antigen ...	82	1e-14
<input type="checkbox"/>	tr Q25571	Outer membrane protein (OMP21) [HP0913] [Helicobacter ...	81	1e-14
<input type="checkbox"/>	tr Q7WV67	Adhesin-binding fucosylated histo-blood group antigen ...	81	1e-14
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<input type="checkbox"/>	tr Q7WV77	Adhesin-binding fucosylated histo-blood group antigen ...	81	2e-14

Graphical overview of the alignments[Click here](#)

to resubmit your query after masking regions matching PROSITE profiles
or Pfam HMMs

([?](#) Help) (use ScanProsite for more details about PROSITE matches)





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Welcome to the SIB BLAST Network Service

If results of this search are reported or published, please mention that the computation was performed at the SIB using the BLAST network service. The SIB BLAST network service uses a server developed at SIB and the NCBI BLAST 2 software.

In case of problems, please read the [online BLAST help](#).
If your question is not covered, please contact [<helpdesk@expasy.org>](mailto:helpdesk@expasy.org).

NCBI BLAST program reference [PMID:9254694]:
Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W., Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. 25:3389-3402(1997).

=====

Query length: 12 AA
Date run: 2004-04-30 21:49:34 UTC+0100 on sib-gml.unil.ch
Program: NCBI BLASTP 1.5.4-Paracel [2003-06-05]
Database: EXPASY/UniProt
1,459,789 sequences; 465,400,423 total letters

[Taxonomic view](#)

[NiceBlast view](#)

[Printable view](#)

List of potentially matching sequences

Send selected sequences to

☐ Include query sequence

Db	AC	Description	Score	E-value
<input type="checkbox"/>	tr Q9ZLY7	Outer membrane protein [JHP0438] [Helicobacter pylori ...	44	3e-04
<input type="checkbox"/>	tr O25230	Hypothetical protein HP0486 [HP0486] [Helicobacter pyl...	44	3e-04
<input type="checkbox"/>	tr Q96EV3	FLJ20896 protein (Fragment) [FLJ20896] [Homo sapiens (...	30	4.1
<input type="checkbox"/>	tr Q86T21	FLJ20896 protein [Homo sapiens (Human)]	30	4.1
<input type="checkbox"/>	tr Q96S75	Graf2 [GRAF-2] [Homo sapiens (Human)]	30	4.1
<input type="checkbox"/>	tr Q8ND72	Hypothetical protein (Fragment) [DKFZP667D142] [Homo s...	30	4.1

Graphical overview of the alignments

to resubmit your query after masking regions matching [PROSITE](#) profiles

or Pfam HMMs

([Help](#)) (use [ScanProsite](#) for more details about PROSITE matches)

Profile hits			
Pfam hits			
	Matches on query sequence		Mat
Submission	1		1
Q9ZLY7			
Q25230			
Q96EV3			
Q86T21			
Q96S75			
Q8ND72			
Submission	1		
Identity	0	25	50 75 100%

Alignments

tr [Q9ZLY7](#) Outer membrane protein [JHP0438] [Helicobacter pylori J99 528 AA
(Campylobacter pylori J99)]

[align](#)

Score = 43.9 bits (96), Expect = 3e-04

Identities = 12/12 (100%), Positives = 12/12 (100%)

Query: 1 VTIEVHGDFINF 12

VTIEVHGDFINF

Sbjct: 30 VTIEVHGDFINF 41

tr [Q25230](#) Hypothetical protein HP0486 [HP0486] [Helicobacter pylori 528 AA
(Campylobacter pylori)]

[align](#)

Score = 43.9 bits (96), Expect = 3e-04

Identities = 12/12 (100%), Positives = 12/12 (100%)

Query: 1 VTIEVHGDFINF 12

VTIEVHGDFINF

Sbjct: 30 VTIEVHGDFINF 41

tr [Q96EV3](#) FLJ20896 protein (Fragment) [FLJ20896] [Homo sapiens (Human)] 629 AA

[align](#)

Score = 29.9 bits (63), Expect = 4.1

Identities = 8/9 (88%), Positives = 8/9 (88%)

Query: 2 TYEVHGDFI 10
TYE HGDFI
Sbjct: 315 TYELHGDFI 323

tr Q86T21 **FLJ20896 protein [Homo sapiens (Human)]** 367 AA

align

Score = 29.9 bits (63), Expect = 4.1
Identities = 8/9 (88%), Positives = 8/9 (88%)

Query: 2 TYEVHGDFI 10
TYE HGDFI
Sbjct: 53 TYELHGDFI 61

tr Q96S75 **Graf2 [GRAF-2] [Homo sapiens (Human)]** 786 AA

align

Score = 29.9 bits (63), Expect = 4.1
Identities = 8/9 (88%), Positives = 8/9 (88%)

Query: 2 TYEVHGDFI 10
TYE HGDFI
Sbjct: 472 TYELHGDFI 480

tr Q8ND72 **Hypothetical protein (Fragment) [DKFZP667D142] [Homo sapiens 333 AA
(Human)]**

align

Score = 29.9 bits (63), Expect = 4.1
Identities = 8/9 (88%), Positives = 8/9 (88%)

Query: 2 TYEVHGDFI 10
TYE HGDFI
Sbjct: 19 TYELHGDFI 27

Database: EXPASY/UniProt

Posted date: Apr 25, 2004 4:51 AM

Number of letters in database: 465,400,423

Number of sequences in database: 1,459,789

Lambda	K	H
0.338	0.287	1.85

Gapped

Lambda	K	H
0.294	0.110	0.610

Matrix: PAM30
Gap Penalties: Existence: 9, Extension: 1
Number of HSP's successfully gapped in prelim test: 0
length of query: 12
length of database: 465,400,423
effective HSP length: 3
effective length of query: 9
effective length of database: 461,021,056
effective search space: 4149189504
effective search space used: 4149189504
T: 16
A: 40
X1: 15 (7.3 bits)
X2: 35 (14.8 bits)
X3: 58 (24.6 bits)
S1: 41 (21.8 bits)
S2: 60 (28.6 bits)

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Hypothetical protein HP0486 [HP0486] [Helicobacter pylori
(Campylobacter pylori)] 528 AA
align

Score = 1100 bits (2846), Expect = 0.0
Identities = 513/513 (100%), Positives = 513/513 (100%)

Query: 16 FTLPLLFTTGS LGAVTYEVHGDFINFAKVGFNHSPINPVKGIYPTETTFVNLTGKLEGSVH 75
FTLPLLFTTGS LGAVTYEVHGDFINFAKVGFNHSPINPVKGIYPTETTFVNLTGKLEGSVH
Sbjct: 16 FTLPLLFTTGS LGAVTYEVHGDFINFAKVGFNHSPINPVKGIYPTETTFVNLTGKLEGSVH 75

Query: 76 LGRGWTVN LGGVLGGQAYDGTKYDRWAKDFTPPSYWDKTSCGTDSMSLCMNATKMWQQSG 135
LGRGWTVN LGGVLGGQAYDGTKYDRWAKDFTPPSYWDKTSCGTDSMSLCMNATKMWQQSG
Sbjct: 76 LGRGWTVN LGGVLGGQAYDGTKYDRWAKDFTPPSYWDKTSCGTDSMSLCMNATKMWQQSG 135

Query: 136 PGGVINPRGIGWEYMGEWNGLFPNYYPANAYLPGGSRRYQVYKANLTYDSDRVHVMVMGRF 195
PGGVINPRGIGWEYMGEWNGLFPNYYPANAYLPGGSRRYQVYKANLTYDSDRVHVMVMGRF
Sbjct: 136 PGGVINPRGIGWEYMGEWNGLFPNYYPANAYLPGGSRRYQVYKANLTYDSDRVHVMVMGRF 195

Query: 196 DITEQEQMDWIYQLFQGFYGTFLTKNMKFLLFSGWGRGIADGQWLFPIYREKPGWVHKA 255
DITEQEQMDWIYQLFQGFYGTFLTKNMKFLLFSGWGRGIADGQWLFPIYREKPGWVHKA
Sbjct: 196 DITEQEQMDWIYQLFQGFYGTFLTKNMKFLLFSGWGRGIADGQWLFPIYREKPGWVHKA 255

Query: 256 GIIYRPTKNLMIHPYVYLIPMVGTLPGAKIEYDTNPEFSGRGIRNRTTFYALYDYRWNNNA 315
GIIYRPTKNLMIHPYVYLIPMVGTLPGAKIEYDTNPEFSGRGIRNRTTFYALYDYRWNNNA
Sbjct: 256 GIIYRPTKNLMIHPYVYLIPMVGTLPGAKIEYDTNPEFSGRGIRNRTTFYALYDYRWNNNA 315

Query: 316 EYGRYAPARYNTWDPFLDNGKWRGLQGPGGATLLLRHHIDINNYFVVGGAYLNIGNPNMN 375
EYGRYAPARYNTWDPFLDNGKWRGLQGPGGATLLLRHHIDINNYFVVGGAYLNIGNPNMN
Sbjct: 316 EYGRYAPARYNTWDPFLDNGKWRGLQGPGGATLLLRHHIDINNYFVVGGAYLNIGNPNMN 375

Query: 376 LGTWGNPVAVDGIEQWVGSIIYSLGFAGIDNITDADAFTEYVKGGGKHGKFSWSVYQRFTT 435
LGTWGNPVAVDGIEQWVGSIIYSLGFAGIDNITDADAFTEYVKGGGKHGKFSWSVYQRFTT
Sbjct: 376 LGTWGNPVAVDGIEQWVGSIIYSLGFAGIDNITDADAFTEYVKGGGKHGKFSWSVYQRFTT 435

Query: 436 APRALEYGIGMYLDYQFSKHVKAGLKLVLWLEFQIRAGYNPGTGFLGPNGQPLNLTGLFE 495
APRALEYGIGMYLDYQFSKHVKAGLKLVLWLEFQIRAGYNPGTGFLGPNGQPLNLTGLFE
Sbjct: 436 APRALEYGIGMYLDYQFSKHVKAGLKLVLWLEFQIRAGYNPGTGFLGPNGQPLNLTGLFE 495

Query: 496 SSAFAQGPQNMGGIAKSITQDRSHLMTHISYSF 528
SSAFAQGPQNMGGIAKSITQDRSHLMTHISYSF
Sbjct: 496 SSAFAQGPQNMGGIAKSITQDRSHLMTHISYSF 528

tr Q9ZLY7 Outer membrane protein [JHP0438] [Helicobacter pylori J99] 528 AA
(Campylobacter pylori J99)
align

Score = 1058 bits (2736), Expect = 0.0
Identities = 488/512 (95%), Positives = 500/512 (97%)

Query: 17 TLPLLFTTGS LGAVTYEVHGDFINFAKVGFNHSPINPVKGIYPTETTFVNLTGKLEGSVHL 76
TLPLLFTTGS LGAVTYEVHGDFINF+KVGFN SPINPVKGIYPTETTFVNLTGKLEGSVHL
Sbjct: 17 TLPLLFTTGS LGAVTYEVHGDFINFSKVGFNRSPINPVKGIYPTETTFVNLTGKLEGSVHL 76

Query: 77 GRGWTVN LGGVLGGQAYDGTKYDRWAKDFTPPSYWDKTSCGTDSMSLCMNATKMWQQSGP 136
GRGWTVN+GGVLGGQ YD T+YDRWAKDFTPPSYWDKTSCGTDS+SLCMNATKMWQQ GP
Sbjct: 77 GRGWTVN VGGVLGGQVYDNTRYDRWAKDFTPPSYWDKTSCGTDSL SLCMNATKMWQQQGP 136

Query: 137 GGVINPRGIGWEYMGWNGLFPNYYPANAYLPGGSRRYQVYKANLTYDSDRVHVMVMGRFD 196
GG+I+PRGIG+ YMGWNGLFPNYYPANAYLPG SRRY+VYKANLTYDSDRVHVMVMGRFD
Sbjct: 137 GGIIDPRGIGYMYMGWNGLFPNYYPANAYLPGHSRRYEVYKANLTYDSDRVHVMVMGRFD 196

Query: 197 ITEQE QMDWIYQLFQGFYGTFLTKNMKFLLFSGWGRGIADGQWLFPIYREKPGVHKAG 256
+TEQE QMDWIYQLFQGFYGTFLTKNMKFLLFSGWGRGIADGQWLFPIYREKPGW+HKAG
Sbjct: 197 VTEQE QMDWIYQLFQGFYGTFLTKNMKFLLFSSWGRGIADGQWLFPIYREKPGWGIHKAG 256

Query: 257 IIYRPTKNLMIHPYVYLIPMVGTLP GAKIEYDTNPEFSGRGIRNRTTFYALYDYRWNNAE 316
IIYRPTKNLMIHPYVYLIPMVGTLP GAKIEYDTNPEFSGRGIRN+TTFY LYDYRWNNAE
Sbjct: 257 IIYRPTKNLMIHPYVYLIPMVGTLP GAKIEYDTNPEFSGRGIRNKTTFYVLYDYRWNNAE 316

Query: 317 YGRYAPARYNTWDPFLDNGKWRGLQGGGATLLLRHHIDINNYFVVGAYLNIGNPNMNL 376
YGRYAPARYNTWDPFLDNGKWRGLQGGGATL L HHIDINNYFVVGAYLNIGNPNMNL
Sbjct: 317 YGRYAPARYNTWDPFLDNGKWRGLQGGGATLYLHHIDINNYFVVGAYLNIGNPNMNL 376

Query: 377 GTWGNPVAVDGIEQWVGSIIYSLGFAGIDNITDADAFTEYVKGGGKHGKFSWSVYQRFTTA 436
GTWGNPVA+DGIEQWVG IYSLGFAGIDNITDADAFTEYVKGGGKHGKFSWSVYQRFTTA
Sbjct: 377 GTWGNPVALDGIEQWVGIIYSLGFAGIDNITDADAFTEYVKGGGKHGKFSWSVYQRFTTA 436

Query: 437 PRALEYGIGMYLDYQFSKHVKAGLKLWLEFQIRAGYNPGTGFLGPNGQPLNLNTGLFES 496
PRALEYGIGMYLDYQFSKHVKAGLKLWLEFQIRAGYNPGTGFLGPNGQPLNLN GLFES
Sbjct: 437 PRALEYGIGMYLDYQFSKHVKAGLKLWLEFQIRAGYNPGTGFLGPNGQPLNLNGLFES 496

Query: 497 SAFAQGPQNMGGIAKSITQDRSHLMTHISYSF 528
SAFAQGPQNMGGIAKSITQDRSHLMTHISYSF
Sbjct: 497 SAFAQGPQNMGGIAKSITQDRSHLMTHISYSF 528

Reconnected in file OS 30apr04 07:30:47

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* ALL NEW CURRENT YEAR RANGES HAVE BEEN * * *
* * * INSTALLED * * *

SYSTEM:OS - DIALOG OneSearch

File 155:MEDLINE(R) 1966-2004/Apr W4

(c) format only 2004 The Dialog Corp.

*File 155: Medline has been reloaded. Accession numbers have changed. Please see HELP NEWS 154 for details.

File 5:Biosis Previews(R) 1969-2004/Apr W4

(c) 2004 BIOSIS

File 34:SciSearch(R) Cited Ref Sci 1990-2004/Apr W4

(c) 2004 Inst for Sci Info

File 35:Dissertation Abs Online 1861-2004/Apr

(c) 2004 ProQuest Info&Learning

File 48:SPORTDiscus 1962-2004/Apr

(c) 2004 Sport Information Resource Centre

File 65:Inside Conferences 1993-2004/Apr W4

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File 71:ELSEVIER BIOBASE 1994-2004/Apr W3

(c) 2004 Elsevier Science B.V.

File 73:EMBASE 1974-2004/Apr W4

(c) 2004 Elsevier Science B.V.

File 91:MANTIS(TM) 1880-2004/Dec

2001 (c) Action Potential

File 94:JICST-EPlus 1985-2004/Apr W2

(c)2004 Japan Science and Tech Corp(JST)

File 98:General Sci Abs/Full-Text 1984-2004/Apr

(c) 2004 The HW Wilson Co.

File 135:NewsRx Weekly Reports 1995-2004/Apr W3

(c) 2004 NewsRx

*File 135: New newsletters are now added. See Help News135 for the complete list of newsletters.

File 144:Pascal 1973-2004/Apr W3

(c) 2004 INIST/CNRS

File 149:TGG Health&Wellness DB(SM) 1976-2004/Apr W3

(c) 2004 The Gale Group

File 156:ToxFile 1965-2004/Apr W4

(c) format only 2004 The Dialog Corporation

File 159:Cancerlit 1975-2002/Oct

(c) format only 2002 Dialog Corporation

*File 159: Cancerlit ceases updating with immediate effect. Please see HELP NEWS.

File 162:Global Health 1983-2004/Mar

(c) 2004 CAB International

File 164:Allied & Complementary Medicine 1984-2004/Apr

(c) 2004 BLHCIS

File 172:EMBASE Alert 2004/Apr W3

(c) 2004 Elsevier Science B.V.

File 266:FEDRIP 2004/Mar

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File 369:New Scientist 1994-2004/Apr W4

(c) 2004 Reed Business Information Ltd.

File 370:Science 1996-1999/Jul W3

(c) 1999 AAAS

*File 370: This file is closed (no updates). Use File 47 for more current information.

File 399:CA SEARCH(R) 1967-2004/UD=14018

(c) 2004 American Chemical Society

*File 399: Use is subject to the terms of your user/customer agreement. Alert feature enhanced for multiple files, etc. See HELP ALERT.

File 434:SciSearch(R) Cited Ref Sci 1974-1989/Dec

(c) 1998 Inst for Sci Info

File 444:New England Journal of Med. 1985-2004/May W1

(c) 2004 Mass. Med. Soc.

File 467:ExtraMED(tm) 2000/Dec

(c) 2001 Informania Ltd.

*File 467: For information about updating status please see Help News467.

Set Items Description

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Cost is in DialUnits

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Set	Items	Description
S1	23	(HOPE OR (HOP (5N) E) OR HOP-E) AND PYLORI
S2	22275	PORIN?
S3	139383	E3-E12
S4	60828	R1-R27
S5	224	S2 AND (S3 OR S4)
S6	165	S5/1995:2004
S7	59	S5 NOT S6

?t s7/9/1-39

7/9/1 (Item 1 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

(c) format only 2004 The Dialog Corp. All rts. reserv.

10329523 PMID: 7824321

[Susceptibility of strict anaerobic bacteria to antibiotics in France: a multicenter study]

Sensibilite aux antibiotiques des anaerobies stricts en France: etude multicentrique.

Grollier G; Mory F; Quentin C; Girard-Pipau F; Tigaud S; Sedallian A; Dubreuil L

Hopitaux universitaires de La Milettrie, Poitiers, France.

Pathologie-biologie (FRANCE) May 1994, 42 (5) p498-504, ISSN 0369-8114 Journal Code: 0265365

Document type: Journal Article; Multicenter Study ; English Abstract

Languages: FRENCH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

During 1992, the in vitro antibiotic susceptibility of 462 anaerobic bacteria was performed in 7 hospitals, by the reference agar dilution method. Among the 222 *Bacteroides fragilis* group strains, only one *Bacteroides fragilis* strain was resistant to imipenem and all betalactams, even combined with betalactamase-inhibitors while metronidazole resistance could not be detected. One major outer membrane protein (probably a porin) was lacking in some of the six amoxicillin-clavulanic acid resistant *Bacteroides fragilis* group strains. Evolution in antibiotic resistance rates could be assessed only for clindamycin and piperacillin whose resistance rates increased to 14 and 15.8 p. cent, respectively. On the whole anaerobic strains resistance rates were: imipenem 0.2, ticarcillin-clavulanic acid 0.5, amoxicillin-clavulanic acid or metronidazole 1.5, piperacillin 9.1, cefotaxime-sulbactam 9.7, cefoxitin 12.8, clindamycin 13.7, cefotaxime 27.2, amoxicillin 45 and ciprofloxacin 70, respectively.

Tags: Comparative Study; Human; In Vitro

Descriptors: *Anti-Bacterial Agents--pharmacology--PD; **Bacteroides fragilis*--drug effects--DE; **Clostridium*--drug effects--DE; **Clostridium difficile*--drug effects--DE; **Peptostreptococcus*--drug effects--DE; Bacteria, Anaerobic--drug effects--DE; Drug Resistance, Microbial; France; **Gram-Negative Bacteria** --drug effects--DE; Gram-Positive Bacteria--drug effects--DE

CAS Registry No.: 0 (Anti-Bacterial Agents)

Record Date Created: 19950214

Record Date Completed: 19950214

7/9/2 (Item 2 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

(c) format only 2004 The Dialog Corp. All rts. reserv.

10224023 PMID: 7927718

Identification of surface-exposed outer membrane antigens of *Helicobacter pylori*.

Doig P; Trust T J
Department of Biochemistry and Microbiology, University of Victoria,
British Columbia, Canada.

Infection and immunity (UNITED STATES) Oct 1994, 62 (10) p4526-33,
ISSN 0019-9567 Journal Code: 0246127

Contract/Grant No.: 1R01AI29927-01A2; AI; NIAID

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Despite the potential significance of surface-localized antigens in the colonization by and disease processes of *Helicobacter pylori*, few such components have been unequivocally identified and/or characterized. To further investigate the surface of this bacterium, monoclonal antibodies (MAbs) to a sarcosine-insoluble outer membrane fraction prepared from *H. pylori* NCTC 11637 were raised. MAbs were selected on the basis of their surface reactivity to whole cells by enzyme-linked immunosorbent assay, immunofluorescence, and immunoelectron microscopy. By use of this selection protocol, 14 surface-reactive MAbs were chosen. These MAbs were used to identify six protein antigens (molecular masses, 80, 60, 51, 50, 48, and 31 kDa), all of which were localized within or associated with the outer membrane. Two of the MAbs recognized the core region of lipopolysaccharide (LPS). Only these two anti-LPS MAbs also recognized the flagellar sheath, indicating a structural difference between the sheath and outer membrane. Three of the protein antigens (80, 60, and 51 kDa) were strain specific, while the other three antigens were present in other strains of *H. pylori*. Both the 51- and 48-kDa antigens were heat modifiable and likely are porins. A conserved 31-kDa protein may represent another species of porin. A method involving sucrose density ultracentrifugation and Triton extraction that allows the preparation of *H. pylori* outer membranes with minimal inner membrane contamination is described. Sodium dodecyl sulfate-polyacrylamide gel electrophoresis analysis showed that the protein content of the *H. pylori* outer membrane is similar structurally to those of other species of *Helicobacter* but markedly different from those of taxonomically related *Campylobacter* spp. and *Escherichia coli*. *H. pylori* also appeared to lack peptidoglycan-associated proteins.

Tags: Support, Non-U.S. Gov't; Support, U.S. Gov't, P.H.S.

Descriptors: Antigens, Bacterial--analysis--AN; *Bacterial Outer Membrane Proteins--analysis--AN; **Helicobacter pylori*--immunology--IM; Animals; Antibodies, Monoclonal--immunology--IM; Antigens, Surface--analysis--AN; Mice; Mice, Inbred BALB C; Molecular Weight

CAS Registry No.: 0 (Antibodies, Monoclonal); 0 (Antigens, Bacterial); 0 (Antigens, Surface); 0 (Bacterial Outer Membrane Proteins)

Record Date Created: 19941104

Record Date Completed: 19941104

7/9/3 (Item 3 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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10168955 PMID: 8057857

The C-terminal sequence conservation between OmpA-related outer membrane proteins and MotB suggests a common function in both gram-positive and gram-negative bacteria, possibly in the interaction of these domains with peptidoglycan.

De Mot R; Vanderleyden J

Molecular microbiology (ENGLAND) Apr 1994, 12 (2) p333-4, ISSN 0950-382X Journal Code: 8712028

Comment in Mol Microbiol. 1995 Jun;16(6) 1269-70; Comment in PMID 8577259

Document type: Letter

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Tags: Comparative Study

Descriptors: Bacterial Outer Membrane Proteins--chemistry--CH; *Bacterial Proteins--chemistry--CH; * Gram-Negative Bacteria --chemistry--CH; *Gram-Positive Bacteria--chemistry--CH; *Peptidoglycan--metabolism--ME; * Porins --chemistry--CH; *Protein Structure, Tertiary; Amino Acid Sequence; Bacterial Outer Membrane Proteins--metabolism--ME; Bacterial Proteins --metabolism--ME; Molecular Sequence Data; Porins --metabolism--ME; Sequence Alignment; Sequence Homology, Amino Acid; Species Specificity
Molecular Sequence Databank No.: GENBANK/L08448; GENBANK/L26052

CAS Registry No.: 0 (Bacterial Outer Membrane Proteins); 0 (Bacterial Proteins); 0 (MotB protein); 0 (Peptidoglycan); 0 (Porins); 134710-89-7 (OprF protein)

Record Date Created: 19940914

Record Date Completed: 19940914

7/9/4 (Item 4 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

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10127809 PMID: 8022741

[Resistance to antibiotics caused by decrease of the permeability in gram-negative bacterial]

Resistance aux antibiotiques par diminution de la permeabilite chez les bacteries a gram negatif.

Nguyen Van J C; Gutmann L

Laboratoire de Microbiologie medicale, Hopital Broussais, Paris.

Presse medicale (Paris, France - 1983) (FRANCE) Mar 19 1994, 23 (11) p522, 527-31, ISSN 0755-4982 Journal Code: 8302490

Document type: Journal Article; Review; Review, Tutorial ; English Abstract

Languages: FRENCH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Due to their outer membrane, Gram negative bacteria are the only germs which can resist antibiotics by a mechanism of reduced permeability. This outer hydrophobic membrane allows hydrophilic molecules to pass only through its aqueous pores. The transmembrane pores have a trimere structure with a monomere component acting as an aqueous channel. Mean pore diameter is 1 to 1.2 nm. Changes in the absolute number of pores or in qualitative function reduce the diffusion of antibiotics entering the cell. This mechanism of reduced permeability can lead to cross resistance to several families of antibiotics. It is difficult to determine the clinical incidence since such resistances are not always detected. The species most often involved are enterobacteria including Klebsiella, Enterobacter, Serratia and Salmonella. For Pseudomonas aeruginosa, resistance to imipenem by reduced permeability results from a deficit in protein D2 and concerns 12 to 15% of the strains identified in French Hospitals. Reduced permeability is particularly effective when associated with another mechanism of resistance allowing the bacteria to express a higher level of resistance. (34 Refs.)

Tags: In Vitro

Descriptors: Anti-Bacterial Agents--pharmacokinetics--PK; *Anti-Infective Agents--pharmacokinetics--PK; *Cell Membrane Permeability--drug effects--DE ; * Gram-Negative Bacteria --drug effects--DE; 4-Quinolones; Cell Membrane --drug effects--DE; Cell Membrane--physiology--PH; Drug Resistance, Microbial; Gram-Negative Bacteria --ultrastructure--UL; Lactams; Porins --pharmacology--PD

CAS Registry No.: 0 (4-Quinolones); 0 (Anti-Bacterial Agents); 0 (Anti-Infective Agents); 0 (Lactams); 0 (Porins)

Record Date Created: 19940802

Record Date Completed: 19940802

7/9/5 (Item 5 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

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10096672 PMID: 8203834

Activity of Bay y3118 against quinolone-susceptible and -resistant gram-negative and gram-positive bacteria.

Piddock L J; Marshall A J; Jin Y F

Department of Infection, University of Birmingham, United Kingdom.

Antimicrobial agents and chemotherapy (UNITED STATES) Mar 1994, 38

(3) p422-7, ISSN 0066-4804 Journal Code: 0315061

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The activity of Bay y3118 against laboratory strains of bacteria, including those with mutations in *gyrA*, with decreased expression of outer membrane proteins, and/or that are multiply resistant, and 121 selected clinical isolates, including highly fluoroquinolone-resistant bacteria from Spain and Argentina, was determined. Bay y3118 was extremely active (MICs, ≤ 1 microgram/ml) against all bacteria, including quinolone-resistant laboratory strains. However, Bay y3118 was less active against 46 of 121 quinolone-resistant clinical isolates, such that ≥ 16 micrograms of Bay y3118 per ml was required to inhibit 3 isolates. The concentration of Bay y3118 required to inhibit DNA synthesis by 50% correlated well with the MIC. Bay y3118 had accumulation kinetics similar to those of previously studied fluoroquinolones, e.g., ciprofloxacin, and there was a 50% decrease in the steady-state concentration in those members of the family Enterobacteriaceae that lacked porin proteins. Magnesium chloride at 20 mM apparently abolished the accumulation of Bay y3118 into *Escherichia coli* and reduced the level of accumulation into other gram-negative bacteria and *Staphylococcus aureus*. Carbonyl cyanide m-chlorophenylhydrazone at 100 microM enhanced the accumulation of Bay y3118 into *E. coli*, but it had a minimal effect on accumulation into *S. aureus*.

Descriptors: Anti-Infective Agents--pharmacology--PD; *Fluoroquinolones; * Gram-Negative Bacteria --drug effects--DE; *Gram-Positive Bacteria--drug effects--DE; *Quinolones--pharmacology--PD; Bacterial Outer Membrane Proteins--biosynthesis--BI; Bacterial Outer Membrane Proteins--genetics--GE; DNA, Bacterial--biosynthesis--BI; Drug Resistance, Microbial; Gram-Negative Bacteria --genetics--GE; Gram-Negative Bacteria --metabolism--ME; Gram-Positive Bacteria--genetics--GE; Gram-Positive Bacteria--metabolism--ME; Kinetics; Microbial Sensitivity Tests; Molecular Sequence Data; Mutation; Phenotype; Quinolones--metabolism--ME

CAS Registry No.: 0 (Anti-Infective Agents); 0 (Bacterial Outer Membrane Proteins); 0 (DNA, Bacterial); 0 (Fluoroquinolones); 0 (Quinolones); 144194-96-7 (Bay Y3118)

Gene Symbol: *gyrA*

Record Date Created: 19940705

Record Date Completed: 19940705

7/9/6 (Item 6 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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10027312 PMID: 8144487

Transport across the bacterial outer membrane.

Nikaido H

Department of Molecular and Cell Biology, University of California, Berkeley 94720.

Journal of bioenergetics and biomembranes (UNITED STATES) Dec 1993, 25

(6) p581-9, ISSN 0145-479X Journal Code: 7701859

Contract/Grant No.: AI-09644; AI; NIAID

Document type: Journal Article; Review; Review, Tutorial

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Diffusion of small molecules across the outer membrane of gram-negative bacteria may occur through protein channels and through lipid bilayer domains. Among protein channels, many examples of trimeric porins, which produce water-filled diffusion channels, are known. Although the channels are nonspecific, the diffusion rates of solutes are often drastically

affected by their gross physicochemical properties, such as size, charge, or lipophilicity, because the channel has a dimension not too different from that of the diffusing solutes. In the last few years, the structures of three such **porins** have been solved by X-ray crystallography. It is now known that a monomer unit traverses the membrane 16 times as beta-strands, and one of the external loop folds back into the channel to produce a narrow constriction. Most of the static properties of the channel, such as the pore size and the position of the amino acids that produce the constriction, can now be explained by the three-dimensional structure. Controversy, however, still surrounds the issue of whether there are dynamic modulation of the channel properties in response to pH, ionic strength, or membrane potential, and of whether such responses are physiological. More recently, two examples of monomeric **porins** have been identified. These **porins** allow a very slow diffusion of solutes, but the reason for this low permeability is still unclear. Finally, channels with specific binding sites facilitate the diffusion of specific classes of nutrients, often those compounds that are too large to penetrate rapidly through the **porin** channels. (ABSTRACT TRUNCATED AT 250 WORDS) (63 Refs.)

Tags: Support, Non-U.S. Gov't; Support, U.S. Gov't, P.H.S.

Descriptors: Bacterial Outer Membrane Proteins--metabolism--ME; *Cell Membrane--metabolism--ME; * **Gram-Negative Bacteria** --metabolism--ME; * **Porins** --metabolism--ME; Bacterial Outer Membrane Proteins--chemistry--CH; Biological Transport; Crystallography, X-Ray; Lipid Bilayers; Models, Molecular; **Porins** --chemistry--CH; Protein Structure, Secondary

CAS Registry No.: 0 (Bacterial Outer Membrane Proteins); 0 (Lipid Bilayers); 0 (Porins)

Record Date Created: 19940505

Record Date Completed: 19940505

7/9/7 (Item 7 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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10012817 PMID: 8132346

Immunobiological activities of Helicobacter pylori porins .

Tufano M A; Rossano F; Catalanotti P; Liguori G; Capasso C; Ceccarelli M T; Marinelli P

Istituto di Microbiologia, Seconda Universita di Napoli, Italy.

Infection and immunity (UNITED STATES) Apr 1994, 62 (4) p1392-9,

ISSN 0019-9567 Journal Code: 0246127

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Studies were carried out on some biological activities of **Helicobacter pylori porins** in vitro. We extracted and purified a **porin** with an apparent molecular mass of 30 kDa. Human polymorphonuclear leukocytes preincubated with **H. pylori porins** showed a decrease of chemotaxis, of adherence to nylon wool, and of chemiluminescence. Used as chemotaxins in place of zymosan-activated serum or as chemotaxinogens in place of zymosan, the **porins** induced polymorphonuclear leukocyte migration. Human monocytes and lymphocytes cultivated in the presence of **H. pylori porins** released cytokines. Release of the various cytokines studied was obtained with differentiated kinetics and at various **porin** concentrations. Starting only 3 h after culture, tumor necrosis factor alpha is released quickly, reaching a peak at 18 h, at a **porin** concentration of 1 microgram/ml/10(6) cells. Interleukin-6 (IL-6) appears later, with a peak at 10 micrograms/ml/10(6) cells, while IL-8 is released after 6 h of culture, with a peak at 24 h, at a **porin** concentration of 10 micrograms/ml/10(6) cells, while IL-8 is released after 6 h of culture, with a peak at 24 h, at a **porin** concentration of 10 micrograms/ml/10(6) cells. Lymphocytes stimulated by **H. pylori porins** release gamma interferon after 18 h of culture at higher concentrations of **porins** (20 micrograms/ml/10(6) cells). Granulocyte macrophage colony-stimulating factor is released from 6 to 48 h at a concentration of 1 microgram/ml/10(6) cells, while both IL-3 and IL-4 are released after 18 h of culture at different **porin** concentrations (0.1 and 1 microgram/ml/10(6) cells, respectively). Our

results lead us to think that during H. pylori infection, surface components, **porins** in particular, are able to induce a series of chain reactions ranging from the inflammatory to the immunological responses.

Tags: Human; Support, Non-U.S. Gov't

Descriptors: **Helicobacter** pylori--pathogenicity--PY; * **Porins** --pharmacology--PD; Chemotaxis, Leukocyte--drug effects--DE; Granulocyte-Macrophage Colony-Stimulating Factor--secretion--SE; Interleukins--secretion--SE; Lymphocytes--drug effects--DE; Lymphocytes--secretion--SE; Monocytes--drug effects--DE; Monocytes--secretion--SE; Neutrophils--drug effects--DE; Neutrophils--immunology--IM; Tumor Necrosis Factor--secretion--SE
CAS Registry No.: 0 (Interleukins); 0 (Porins); 0 (Tumor Necrosis Factor); 83869-56-1 (Granulocyte-Macrophage Colony-Stimulating Factor)

Record Date Created: 19940421

Record Date Completed: 19940421

7/9/8 (Item 8 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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09974680 PMID: 7508433

Porins and specific diffusion channels in bacterial outer membranes.

Nikaido H

Department of Molecular and Cell Biology, University of California, Berkeley 94720.

Journal of biological chemistry (UNITED STATES) Feb 11 1994, 269 (6) p3905-8, ISSN 0021-9258 Journal Code: 2985121R

Contract/Grant No.: AI-09644; AI; NIAID

Document type: Journal Article; Review; Review, Tutorial

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

(47 Refs.)

Tags: Support, Non-U.S. Gov't; Support, U.S. Gov't, P.H.S.

Descriptors: Bacterial Outer Membrane Proteins; * **Gram-Negative Bacteria** --physiology--PH; *Ion Channels; * **Porins** ; Biological Transport; Diffusion ; Models, Molecular; Protein Structure, Secondary; Protein Structure, Tertiary; Structure-Activity Relationship

CAS Registry No.: 0 (Bacterial Outer Membrane Proteins); 0 (Ion Channels); 0 (Porins)

Gene Symbol: lamB; ompC; ompF; oprB; oprD; phoE; tsx

Record Date Created: 19940317

Record Date Completed: 19940317

7/9/9 (Item 9 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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09751536 PMID: 8391435

Outer-membrane porins from gram-negative bacteria stimulate platelet-activating-factor biosynthesis by cultured human endothelial cells.

Tufano M A; Biancone L; Rossano F; Capasso C; Baroni A; De Martino A; Iorio E L; Silvestro L; Camussi G

Istituto di Micobiologia, Facolta di Medicina e Chirurgia, Seconda Universita di Napoli, Italy.

European journal of biochemistry / FEBS (GERMANY) Jun 15 1993, 214 (3) p685-93, ISSN 0014-2956 Journal Code: 0107600

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Porins are a family of hydrophobic proteins located in the outer membrane of the cell wall in Gram-negative bacteria. The effect of **porins** on the biosynthesis of platelet-activating factor (PAF) by cultured human umbilical-cord-vein-derived endothelial cells (HUVEC) was investigated. The

results demonstrate that **porins** were able to induce a dose-dependent synthesis of PAF in HUVEC. PAF, synthesized after stimulation with **porins**, was mainly cell associated and the synthesis peaked at 15 min, decreasing rapidly thereafter. Experiments with radiolabeled precursors demonstrated that PAF, a 1-O-alkyl-2-acetyl-sn-glycerol-3-phosphorylcholine, was synthesized via the remodeling pathway involving the acetylation of 1-O-alkyl-2-lyso-sn-glycerol-3-phosphorylcholine (2-lysoPAF) generated from 1-O-alkyl-2-acyl-sn-glycerol-3-phosphorylcholine by phospholipase-A2 activity. The activation of phospholipase A2 in HUVEC stimulated by **porins** was detected by observing the mobilization of [¹⁴C]arachidonic acid. In addition, the activity of acetyl-CoA:1-alkyl-sn-glycerol-3-phosphorylcholine 2-O-acetyltransferase was transiently increased in **porin**-stimulated HUVEC and, after incubation with [³H]CoASAc or [³H]acetate, the [³H]acetyl group was incorporated into newly synthesized PAF. **Porins**, by forming transmembrane channels, induced a sustained influx of extracellular ⁴⁵Ca²⁺ into the cytosol. The activation of PAF synthesis by **porins** depended on this influx rather than on intracellular calcium mobilization, since PAF synthesis did not occur in the absence of extracellular Ca²⁺.

Tags: Human; Support, Non-U.S. Gov't

Descriptors: Bacterial Outer Membrane Proteins--pharmacology--PD; *Endothelium, Vascular--metabolism--ME; * **Gram-Negative Bacteria** --chemistry--CH; *Platelet Activating Factor--biosynthesis--BI; Acetyltransferases--metabolism--ME; Calcium--metabolism--ME; Cells, Cultured; Endothelium, Vascular--drug effects--DE; Phospholipases A --metabolism--ME; Platelet Activating Factor--analogs and derivatives--AA; Platelet Activating Factor--metabolism--ME; **Porins**; Salmonella typhimurium; Umbilical Veins

CAS Registry No.: 0 (Bacterial Outer Membrane Proteins); 0 (O-deacetyl platelet activating factor); 0 (Platelet Activating Factor); 0 (Porins); 7440-70-2 (Calcium)

Enzyme No.: EC 2.3.1. (Acetyltransferases); EC 2.3.1.67 (1-alkylglycerophosphocholine acetyltransferase); EC 3.1.1.- (Phospholipases A)

Record Date Created: 19930803

Record Date Completed: 19930803

7/9/10 (Item 10 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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09577939 PMID: 1283000

Purification of *Aeromonas hydrophila* major outer-membrane proteins: N-terminal sequence analysis and channel-forming properties.

Jeanteur D; Gletsu N; Pattus F; Buckley J T

European Molecular Biology Laboratory, Heidelberg, Germany.

Molecular microbiology (ENGLAND) Nov 1992, 6 (22) p3355-63, ISSN

0950-382X Journal Code: 8712028

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Four outer-membrane proteins of *Aeromonas hydrophila* were purified and their N-terminal sequences and channel-forming properties were determined. Three could be matched with proteins from other species. One was a maltoporin, as its level increased when cells were grown in maltose-containing media, and the channel it formed was blocked by maltose. Another was like OmpF and OmpC of *Escherichia coli*, except that its channel fluctuated much more rapidly. The third protein, which was produced in low-phosphate medium, exhibited several properties of the general anion **porin** PhoE. The fourth showed no similarity to any known proteins. It had a unique N-terminus and it formed small sharply-defined cation-selective channels. Two other proteins which corresponded to OmpW of *Vibrio cholerae* and *E. coli* OmpA were partly characterized.

Tags: Comparative Study; Support, Non-U.S. Gov't

Descriptors: **Aeromonas hydrophila*--chemistry--CH; *Bacterial Outer Membrane Proteins--isolation and purification--IP; *Ion Channels; Amino Acid Sequence; Bacterial Outer Membrane Proteins--chemistry--CH; Consensus

Sequence; **Gram-Negative Bacteria** --genetics--GE; Molecular Sequence Data; Molecular Weight; Multigene Family; Sequence Alignment; Sequence Homology, Amino Acid

CAS Registry No.: 0 (Bacterial Outer Membrane Proteins); 0 (Ion Channels)

Gene Symbol: lamB; ompC; ompF; phoE; scrY

Record Date Created: 19930217

Record Date Completed: 19930217

7/9/11 (Item 11 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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09459429 PMID: 1328059

Immunochemical and biological characterization of outer membrane proteins of Porphyromonas endodontalis.

Ogawa T; Kuribayashi S; Shimauchi H; Toda T; Hamada S

Department of Oral Microbiology, Osaka University Faculty of Dentistry, Japan.

Infection and immunity (UNITED STATES) Nov 1992, 60 (11) p4528-33, ISSN 0019-9567 Journal Code: 0246127

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Outer membrane proteins (OMP) of *Porphyromonas endodontalis* HG 370 (ATCC 35406) were prepared from the cell envelope fraction of the organisms. The cell envelope that had been obtained by sonication of the whole cells was extracted in 2% lithium dodecyl sulfate and then successively chromatographed with Sephacryl S-200 HR and DEAE-Sepharose Fast Flow. Two OMP fractions, OMP-I and OMP-II, were obtained, and their immunochemical properties and induction of specific antibodies were examined. The OMP-I preparation consisted of a major protein with an apparent molecular mass of 31 kDa and other moderate to minor proteins of 40.3, 51.4, 67, and 71.6 kDa, while the OMP-II preparation contained 14-, 15.5-, 27-, and 44-kDa proteins as revealed by sodium dodecyl sulfate-polyacrylamide gel electrophoretic analysis. OMP-I was found to form hydrophilic diffusion pores by incorporation into artificial liposomes composed of egg yolk phosphatidylcholine and dicetylphosphate, indicating that OMP-I exhibited significant **porin** activity. However, the liposomes containing heat-denatured OMP-I were scarcely active. Spontaneous and antigen-specific immunoglobulin M (IgM)-, IgG-, and IgA-secreting spot-forming cells (SFC) enzymatically dissociated into single-cell suspensions from chronically inflamed periapical tissues and were enumerated by enzyme-linked immunospot assay. In patients with radicular cysts or dental granulomas, the major isotype of spontaneous SFC was IgG. In radicular cysts, the OMP-II-specific IgG SFC represented 0.13% of the total IgG SFC, while the antigen-specific IgA or IgM SFC was not observed. It was also found that none of these mononuclear cells produced antibodies specific for OMP-I or lipopolysaccharide of *P. endodontalis*.

Tags: Human

Descriptors: Antibodies, Bacterial--immunology--IM; *Bacterial Outer Membrane Proteins--immunology--IM; * **Gram-Negative Bacteria** --immunology--IM; *Periapical Abscess--microbiology--MI; Bacterial Outer Membrane Proteins--isolation and purification--IP; **Gram-Negative Bacteria** --chemistry--CH; Leukocytes, Mononuclear--immunology--IM; Lipopolysaccharides--chemistry--CH; Lipopolysaccharides--immunology--IM; Periapical Granuloma--immunology--IM; **Porins** ; Radicular Cyst--immunology--IM

CAS Registry No.: 0 (Antibodies, Bacterial); 0 (Bacterial Outer Membrane Proteins); 0 (Lipopolysaccharides); 0 (Porins)

Record Date Created: 19921125

Record Date Completed: 19921125

7/9/12 (Item 12 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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09327784 PMID: 1601751

Factors involved in the enhanced efficacy against gram-negative bacteria of fourth generation cephalosporins.

Hancock R E; Bellido F

Canadian Bacterial Diseases Network, University of British Columbia, Vancouver.

Journal of antimicrobial chemotherapy (ENGLAND) Apr 1992, 29 Suppl A p1-6, ISSN 0305-7453 Journal Code: 7513617

Document type: Journal Article; Review; Review, Tutorial

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The fourth generation cephalosporins, cefpirome and cefepime, demonstrate better activity against strains of *Enterobacter cloacae* with derepressed beta-lactamase than the third generation compounds cefotaxime and ceftriaxone. Several methodological refinements were used to measure the parameters, predicted by the Zimmermann-Rosselet equation to be important in the efficacy of beta-lactams. Outer membrane permeability was measured by a novel HPLC method. The kinetics of interaction of purified beta-lactamase with beta-lactams were estimated to calculate the inhibition and catalytic constants. The periplasmic concentration of beta-lactams leading to growth inhibition of cells was determined by substituting the above parameters into the Zimmermann-Rosselet equation. Consideration of these three factors allowed accurate prediction of MICs in isogenic *E. cloacae* strains with differing **porin** or beta-lactamase contents. The fourth generation cephalosporins had markedly reduced affinity for beta-lactamase and increased outer membrane permeability when compared to the third generation cephalosporins. Such advantages were only partly offset by a lower stability of complexes with beta-lactamase and reduced affinity for their targets. (13 Refs.)

Tags: Comparative Study; Support, Non-U.S. Gov't

Descriptors: Anti-Bacterial Agents--pharmacology--PD; *Cephalosporins--pharmacology--PD; * **Gram-Negative Bacteria** --drug effects--DE; Anti-Bacterial Agents--metabolism--ME; Cell Membrane Permeability; **Gram-Negative Bacteria** --metabolism--ME; Hydrolysis; Kinetics; Microbial Sensitivity Tests

CAS Registry No.: 0 (Anti-Bacterial Agents); 0 (Cephalosporins)

Record Date Created: 19920714

Record Date Completed: 19920714

7/9/13 (Item 13 from file: 155)

DIALOG(R) File 155: MEDLINE(R)

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09260069 PMID: 1373289

Topology of the anion-selective porin Omp32 from *Comamonas acidovorans*.

Gerbl-Rieger S; Engelhardt H; Peters J; Kehl M; Lottspeich F; Baumeister W

Max Planck Institut fur Biochemie, Martinsried, Federal Republic of Germany.

Journal of structural biology (UNITED STATES) Jan-Feb 1992, 108 (1) p14-24, ISSN 1047-8477 Journal Code: 9011206

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Limited proteolysis experiments were performed with outer membranes from *Comamonas acidovorans* to probe the topology of its major protein component, the anion-selective **porin** Omp32. Proteinase K treatment above a critical temperature of 42 degrees C cleaved the surface-exposed regions of the **porin**, yielding membrane-embedded fragments which were separated by SDS polyacrylamide gel electrophoresis or reversed phase chromatography. The identification of the proteinase K-sensitive sites was performed by microsequencing. This allowed us to determine six surface-exposed sites of the **porin**, all located in nonconserved primary structure regions. These

results along with the previously determined amino acid sequence and in conjunction with some structural constraints applicable to **porins** allowed us to propose a chain-folding model of the Omp32 **porin**. The features of our model are compared with the structure of the Rhodobacter capsulatus **porin**, recently established by X-ray crystallography (Weiss et al., 1991) and they are used to elucidate the structural basis of the anion selectivity.

Tags: Support, Non-U.S. Gov't
Descriptors: Bacterial Outer Membrane Proteins--ultrastructure--UL; ***Gram-Negative Bacteria** --ultrastructure--UL; *Ion Channels--ultrastructure--UL; Amino Acid Sequence; Bacterial Outer Membrane Proteins--chemistry--CH; Bacterial Outer Membrane Proteins--metabolism--ME; Blotting, Western; Calorimetry, Differential Scanning; Cations; Electrophoresis, Polyacrylamide Gel; Endopeptidase K; Ion Channels--chemistry--CH; Microscopy, Electron; Molecular Sequence Data; Peptide Fragments--chemistry--CH; **Porins**; Protein Conformation; Serine Endopeptidases--metabolism--ME; Spectrophotometry, Infrared
CAS Registry No.: 0 (Bacterial Outer Membrane Proteins); 0 (Cations); 0 (Ion Channels); 0 (Omp32 protein); 0 (Peptide Fragments); 0 (Porins)
Enzyme No.: EC 3.4.21 (Serine Endopeptidases); EC 3.4.21.64 (Endopeptidase K)
Record Date Created: 19920515
Record Date Completed: 19920515

7/9/14 (Item 14 from file: 155)
DIALOG(R) File 155:MEDLINE(R)
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09257258 PMID: 1373213
Porins and specific channels of bacterial outer membranes.
Nikaido H
Department of Molecular and Cell Biology, University of California, Berkeley 94720.
Molecular microbiology (ENGLAND) Feb 1992, 6 (4) p435-42, ISSN 0950-382X Journal Code: 8712028
Contract/Grant No.: AI-09644; AI; NIAID
Document type: Journal Article; Review; Review, Tutorial
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS

Porins and specific channels both produce water-filled pores that allow the transmembrane diffusion of small solutes, but the latter contain specific ligand-binding sites within the channels. Recent structural studies show that many or most of these proteins exist as beta-barrels with the beta-strands traversing the thickness of the outer membrane. The channels often have diameters in the range of 1 nm, and thus the penetration rates of solutes through **porin** channels are likely to be affected strongly by what appear to be minor differences in the size, shape, hydrophobicity or charge of the solute molecule. With the specific channels, the presence of binding sites can accelerate very significantly the diffusion of some ligands when they are present at low concentrations. Thus these simple channels can sometimes achieve a surprising degree of real or apparent specificity. Recent data tend to favour the idea that these proteins are first exported into the periplasm, and then inserted into the outer membrane. Although lipopolysaccharides seem to play a significant role in the final assembly of the trimeric **porins**, the details of the targeting process still remain to be elucidated. (58 Refs.)

Tags: Support, U.S. Gov't, P.H.S.
Descriptors: *Bacterial Outer Membrane Proteins--chemistry--CH; *Ion Channels--chemistry--CH; Amino Acid Sequence; Antibodies--immunology--IM; Bacterial Outer Membrane Proteins--metabolism--ME; **Gram-Negative Bacteria** --chemistry--CH; **Gram-Negative Bacteria** --metabolism--ME; Ion Channels --metabolism--ME; Lipopolysaccharides--metabolism--ME; Molecular Sequence Data; **Porins**; Protein Conformation
CAS Registry No.: 0 (Antibodies); 0 (Bacterial Outer Membrane Proteins); 0 (Ion Channels); 0 (Lipopolysaccharides); 0 (Porins)

Record Date Created: 19920514
Record Date Completed: 19920514

7/9/15 (Item 15 from file: 155)
DIALOG(R) File 155:MEDLINE(R)
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09152700 PMID: 1662760

The bacterial porin superfamily: sequence alignment and structure prediction.

Jeanteur D; Lakey J H; Pattus F
European Molecular Biology Laboratory, Heidelberg, Germany.
Molecular microbiology (ENGLAND) Sep 1991, 5 (9) p2153-64, ISSN
0950-382X Journal Code: 8712028
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS

The **porins** of Gram-negative bacteria are responsible for the 'molecular sieve' properties of the outer membrane. They form large water-filled channels which allow the diffusion of hydrophilic molecules into the periplasmic space. Owing to the strong hydrophilicity of their amino acid sequence and the nature of their secondary structure (beta strands), conventional hydropathy methods for predicting membrane topology are useless for this class of protein. The large number of available **porin** amino acid sequences was exploited to improve the accuracy of the prediction in combination with tools detecting amphipathicity of secondary structure. Using the constraints of beta-sheet structure these **porins** are predicted to contain 16 membrane-spanning strands, 14 of which are common to the two (enteric and the neisserial) **porin** subfamilies.

Descriptors: Bacterial Outer Membrane Proteins--chemistry--CH; *
Gram-Negative Bacteria --chemistry--CH; Amino Acid Sequence; Bacterial Outer Membrane Proteins--genetics--GE; Biological Transport; Escherichia coli--chemistry--CH; Escherichia coli--genetics--GE; **Gram-Negative Bacteria** --genetics--GE; Molecular Sequence Data; Phylogeny; **Porins** ; Protein Conformation; Rhodobacter capsulatus--chemistry--CH; Rhodobacter capsulatus--genetics--GE; Sequence Homology, Nucleic Acid; Surface Properties

CAS Registry No.: 0 (Bacterial Outer Membrane Proteins); 0 (Porins)
Gene Symbol: Lc; Nmpc; OmpC; OmpF; P2; PIA1; PIB1; PIB2; PhoE; PorA; PorA1

Record Date Created: 19920219
Record Date Completed: 19920219

7/9/16 (Item 16 from file: 155)
DIALOG(R) File 155:MEDLINE(R)
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08982908 PMID: 1864283

Impermeability to quinolones in gram-positive and gram-negative bacteria.
Bryan L E; Bedard J
Department of Microbiology, University of Calgary, Canada.
European journal of clinical microbiology & infectious diseases -
official publication of the European Society of Clinical Microbiology (GERMANY) Apr 1991, 10 (4) p232-9, ISSN 0934-9723 Journal Code:
8804297

Document type: Journal Article; Review; Review, Tutorial
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS

The initial step in the accumulation of fluoroquinolone antimicrobial agents is binding to cell surface components reduced by lowered pH and divalent cations. Uptake into gram-negative and gram-positive bacteria is by simple diffusion. Entry through the outer membrane occurs preferentially for most agents by the **porin** route but a second process using the

self-promoted uptake pathway is active especially for more hydrophobic agents. Fluoroquinolones bind to vesicles of phospholipid which may be the initiating step in cross-cytoplasmic membrane diffusion. An active efflux system has been described in Escherichia coli with evidence supporting its presence in several other bacteria. Total upset is not altered by a resistant gyrase. Resistant isolates associated with reduced total quinolone accumulation due to lowered uptake have been described for laboratory mutants and clinical isolates. Most but not all of these have had alterations in outer membrane proteins. A functionally dominant resistance gene has been cloned from resistant Staphylococcus aureus and codes for a highly hydrophobic protein most likely membrane associated. This gene is expressed in Escherichia coli and specifies resistance especially to hydrophilic quinolones, possibly by altered accumulation. (40 Refs.)

Descriptors: Anti-Infective Agents--metabolism--ME; * **Gram-Negative Bacteria** --metabolism--ME; *Gram-Positive Bacteria--metabolism--ME; 4-Quinolones; Anti-Infective Agents--pharmacology--PD; Bacterial Outer Membrane Proteins--metabolism--ME; Cell Membrane Permeability; Drug Resistance, Microbial; **Gram-Negative Bacteria** --drug effects--DE; Gram-Positive Bacteria--drug effects--DE; Models, Biological

CAS Registry No.: 0 (4-Quinolones); 0 (Anti-Infective Agents); 0 (Bacterial Outer Membrane Proteins)

Record Date Created: 19910912

Record Date Completed: 19910912

7/9/17 (Item 17 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

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08877878 PMID: 1965316

Antibiotic permeation through the bacterial outer membrane.

Georgopapadakou N H

Roche Research Center, Nutley NJ 07110.

Journal of chemotherapy (Florence, Italy) (ITALY) Oct 1990, 2 (5) p275-9, ISSN 1120-009X Journal Code: 8907348

Document type: Journal Article; Review; Review, Tutorial

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

(55 Refs.)

Descriptors: Anti-Bacterial Agents--pharmacokinetics--PK; *Bacterial Outer Membrane Proteins--metabolism--ME; * **Gram-Negative Bacteria** --metabolism--ME; Aminoglycosides; Cell Membrane Permeability; **Gram-Negative Bacteria** --drug effects--DE; Lactams; **Porins**

CAS Registry No.: 0 (Aminoglycosides); 0 (Anti-Bacterial Agents); 0 (Bacterial Outer Membrane Proteins); 0 (Lactams); 0 (Porins)

Record Date Created: 19910603

Record Date Completed: 19910603

7/9/18 (Item 18 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

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08838075 PMID: 1848840

Nucleotide and derived amino acid sequences of the major porin of Comamonas acidovorans and comparison of porin primary structures.

Gerbl-Rieger S; Peters J; Kellermann J; Lottspeich F; Baumeister W

Max-Planck Institut fur Biochemie, Martinsried bei Munchen, Federal Republic of Germany.

Journal of bacteriology (UNITED STATES) Apr 1991, 173 (7) p2196-205, ISSN 0021-9193 Journal Code: 2985120R

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The DNA sequence of the gene which codes for the major outer membrane **porin** (Omp32) of *Comamonas acidovorans* has been determined. The structural gene encodes a precursor consisting of 351 amino acid residues with a signal peptide of 19 amino acid residues. Comparisons with amino acid sequences of outer membrane proteins and **porins** from several other members of the class Proteobacteria and of the *Chlamydia trachomatis* **porin** and the *Neurospora crassa* mitochondrial **porin** revealed a motif of eight regions of local homology. The results of this analysis are discussed with regard to common structural features of **porins**.

Tags: Comparative Study

Descriptors: Bacterial Outer Membrane Proteins--genetics--GE; *Genes, Structural, Bacterial; * **Gram-Negative Bacteria** --genetics--GE; Amino Acid Sequence; Bacterial Outer Membrane Proteins--chemistry--CH; Base Sequence; Cloning, Molecular; DNA, Bacterial--genetics--GE; Molecular Sequence Data; **Porins**

CAS Registry No.: 0 (Bacterial Outer Membrane Proteins); 0 (DNA, Bacterial); 0 (Omp32 protein); 0 (Porins)

Gene Symbol: MOMP; Omp32; OmpA; OmpC; OmpF; P1B; PhoE

Record Date Created: 19910430

Record Date Completed: 19910430

7/9/19 (Item 19 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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08785876 PMID: 2280690

A rapid method for reconstitution of bacterial membrane proteins.

Varadhachary A; Maloney P C

Department of Physiology, Johns Hopkins School of Medicine, Baltimore, Maryland 21205.

Molecular microbiology (ENGLAND) Aug 1990, 4 (8) p1407-11, ISSN 0950-382X Journal Code: 8712028

Contract/Grant No.: GM24195; GM; NIGMS

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

We have devised a simple method for the reconstitution of bacterial membrane proteins directly from small (1-20 ml) volumes of cell culture, thus eliminating the preparation of membrane vesicles. Cells are subjected to simultaneous lysozyme digestion and osmotic lysis, and after brief centrifugation ghosts are solubilized in 1.2% octyl-beta-D-glucopyranoside (octylglucoside) in the presence of added carrier lipid and an osmolyte. Aliquots of the clarified supernatant are suitable for reconstitution, as documented by using extracts from three different Gram-negative cells to recover both inorganic phosphate (Pi)-linked antiport and oxalate:formate exchange activities in proteoliposomes. These proteoliposomes are physically stable, non-leaky and can sustain a membrane potential and, because functional **porins** do not reconstitute, the artificial system has transport characteristics similar to those found when proteoliposomes are obtained using standard methods. This method should become an important tool for the screening and characterization of large numbers of strains, both wild-type and mutant.

Tags: Support, U.S. Gov't, Non-P.H.S.; Support, U.S. Gov't, P.H.S.

Descriptors: Bacterial Proteins; * **Gram-Negative Bacteria** --analysis--AN; *Membrane Proteins; *Proteolipids; Bacterial Proteins--metabolism--ME; Bacteriolysis; Biological Transport; Cell Membrane--chemistry--CH; Centrifugation; **Gram-Negative Bacteria** --ultrastructure--UL; Ion Exchange; Membrane Potentials; Membrane Proteins--metabolism--ME; Methods; Muramidase --metabolism--ME; Phosphates--metabolism--ME; Proteolipids--metabolism--ME

CAS Registry No.: 0 (Bacterial Proteins); 0 (Membrane Proteins); 0 (Phosphates); 0 (Proteolipids); 0 (proteoliposomes)

Enzyme No.: EC 3.2.1.17 (Muramidase)

Record Date Created: 19910313

Record Date Completed: 19910313

7/9/20 (Item 20 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

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08696527 PMID: 2228824

In-vitro antibacterial activity of DQ-2556 and its stability to various beta-lactamases.

Fujimoto T; Watanabe M; Inoue M; Mitsuhashi S

Episome Institute, Seta-gun, Japan.

Journal of antimicrobial chemotherapy (ENGLAND) Sep 1990, 26 (3)
p329-41, ISSN 0305-7453 Journal Code: 7513617

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

DQ-2556, a new cephalosporin, showed a broad antibacterial spectrum over Gram-positive and -negative organisms. The activity of DQ-2556 against recent clinical isolates of Gram-positive cocci and Enterobacteriaceae was comparable with that of cefpirome, and superior to that of ceftazidime. DQ-2556 was almost as active as cefpirome against *Pseudomonas aeruginosa*, but was less active than ceftazidime. With the exception of *Ps. aeruginosa*, DQ-2556 was bactericidal against various organisms at either the MIC or twice the MIC. DQ-2556 bound preferentially to penicillin-binding proteins (PBPs) 2, 1 and 3 of *Staphylococcus aureus*, PBPs 3, 1A and 1B of *Escherichia coli* and PBPs 1A, 3 and 4 of *Ps. aeruginosa*. DQ-2556 was stable to various penicillinases and cephalosporinases, but was unstable to oxyiminocephalosporinases. The Km values of DQ-2556 for the cephalosporinases of *Citrobacter freundii* and *Enterobacter cloacae* were only two- or three-fold higher than those of ceftazidime, indicating that DQ-2556 had a relatively high affinity for these enzymes compared with other recently developed cephalosporins. The MIC of DQ-2556 for *Esch. coli* increased four-fold in an OmpF-deficient mutant, indicating that the OmpF porin was one of the major routes for penetration of DQ-2556 into *Esch. coli* cells.

Tags: Comparative Study

Descriptors: Cephalosporins--pharmacology--PD; *Enterobacteriaceae--drug effects--DE; * Gram-Negative Bacteria --drug effects--DE; *Gram-Positive Bacteria--drug effects--DE; Ceftazidime--pharmacology--PD; Cephalosporins --metabolism--ME; Drug Stability; Gram-Negative Bacteria --enzymology--EN; Gram-Positive Bacteria--enzymology--EN; Microbial Sensitivity Tests; beta-Lactamases--metabolism--ME

CAS Registry No.: 0 (Cephalosporins); 102253-70-3 (DQ 2556); 78439-06-2 (Ceftazidime); 84957-29-9 (cefpirome)

Enzyme No.: EC 3.5.2.6 (beta-Lactamases)

Record Date Created: 19901204

Record Date Completed: 19901204

7/9/21 (Item 21 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

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08316851 PMID: 2808204

Antibacterial activity of meropenem against gram-negative bacteria with a permeability defect and against staphylococci.

Kitzis M D; Acar J F; Gutmann L

Laboratoire de Microbiologie, Hopital Saint Joseph, Paris, France.

Journal of antimicrobial chemotherapy (ENGLAND) Sep 1989, 24 Suppl A
p125-32, ISSN 0305-7453 Journal Code: 7513617

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Meropenem, like imipenem, showed a good affinity for high molecular weight PBPs of *Escherichia coli* and *Pseudomonas aeruginosa* and had a better affinity for PBP3 than imipenem. Meropenem, like imipenem, also remained almost fully active against permeability mutants of enterobacteria lacking

in confirmed or putative **porins**. This good permeation of the carbapenems may relate to their zwitterionic character. In-vitro, mutants and clinical isolates of *P. aeruginosa*, for which the MIC of imipenem was greater than or equal to 4 mg/l, were always more sensitive to meropenem. Methicillin resistant staphylococci were sensitive neither to imipenem nor to meropenem.

Descriptors: Bacterial Proteins; *Carbapenems--pharmacology--PD; *Cell Membrane Permeability--drug effects--DE; * **Gram-Negative Bacteria** --drug effects--DE; *Hexosyltransferases; *Peptidyltransferase; *Staphylococcus --drug effects--DE; *Thienamycins--pharmacology--PD; Carbapenems --metabolism--ME; Carrier Proteins--metabolism--ME; Culture Media; Drug Resistance, Microbial; Enterobacteriaceae--drug effects--DE; **Gram-Negative Bacteria** --genetics--GE; **Gram-Negative Bacteria** --metabolism--ME; Imipenem--metabolism--ME; Imipenem--pharmacology--PD; Microbial Sensitivity Tests; Muramoylpentapeptide Carboxypeptidase--metabolism--ME; Thienamycins--metabolism--ME

CAS Registry No.: 0 (Bacterial Proteins); 0 (Carbapenems); 0 (Carrier Proteins); 0 (Culture Media); 0 (Thienamycins); 74431-23-5 (Imipenem); 96036-03-2 (meropenem)
Enzyme No.: EC 2.3.2.12 (Peptidyltransferase); EC 2.4.1.- (Hexosyltransferases); EC 3.4.16.4 (penicillin-binding protein); EC 3.4.17.8 (Muramoylpentapeptide Carboxypeptidase)
Record Date Created: 19891219
Record Date Completed: 19891219

7/9/22 (Item 22 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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08306551 PMID: 2552981

Interaction of fluid phase C1/C1q and macrophage membrane-associated C1q with gram-negative bacteria.

Clas F; Euteneuer B; Stemmer F; Loos M
Institute of Medical Microbiology, University of Mainz, W.-Germany.
Behring Institute Mitteilungen (GERMANY, WEST) Jul 1989, (84)
p236-54, ISSN 0301-0457 Journal Code: 0367532
Document type: Journal Article; Review; Review, Tutorial
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS

Many gram-negative bacteria are killed after treatment with normal non-immune sera and directly bind and activate C1 in the absence of antibodies. For the immediate killing of such serum-sensitive bacteria, like R-forms of *Salmonella* strains, all serum complement components are essential. When purified serum C1 to C9 are used, further activation of the cascade requires an additional serum factor. This glycoprotein differs from antibody and mediates the attachment of C4b to the bacterial cell surface. The antibody-independent interaction with C1 occurs via C1q, which binds to LPS. In addition outer membrane proteins bind C1q and C1. The association of these **porins** with LPS may potentiate the antibody-independent C1q and C1 binding to serum-sensitive bacteria. **Porins** can contribute to complement activation mainly through the classical pathway. LPS and **porins** from bacterial cell walls are also involved in the binding of gram-negative bacteria to macrophages. This antibody-independent attachment and ingestion of gram-negative bacteria is mediated by endogenous macrophage-membrane associated C1q. (71 Refs.)

Tags: Human

Descriptors: Blood Bactericidal Activity; *Complement 1--metabolism--ME; *Complement 1q--metabolism--ME; * **Gram-Negative Bacteria** ; *Macrophages --metabolism--ME; *Membrane Proteins--metabolism--ME; Animals; Bacterial Outer Membrane Proteins--isolation and purification--IP; Bacterial Outer Membrane Proteins--metabolism--ME; Cell Wall; Complement Activation; Complement Membrane Attack Complex--metabolism--ME; Lipopolysaccharides --metabolism--ME; Phagocytosis; **Porins** ; *Salmonella*--classification--CL
CAS Registry No.: 0 (Bacterial Outer Membrane Proteins); 0 (Complement 1); 0 (Complement Membrane Attack Complex); 0 (Lipopolysaccharides); 0 (Membrane Proteins); 0 (Porins); 80295-33-6 (Complement 1q)

Record Date Created: 19891115
Record Date Completed: 19891115

7/9/23 (Item 23 from file: 155)
DIALOG(R) File 155:MEDLINE(R)
(c) format only 2004 The Dialog Corp. All rts. reserv.

08042937 PMID: 2537696

Quinolone antimicrobial agents: mechanism of action and resistance development.

Bryan L E; Bedard J; Wong S; Chamberland S
Department of Microbiology and Infectious Diseases, Faculty of Medicine,
University of Calgary, Alberta.

Clinical and investigative medicine. Medecine clinique et experimentale (CANADA) Feb 1989, 12 (1) p14-9, ISSN 0147-958X Journal Code: 7804071

Document type: Journal Article; Review; Review, Tutorial

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The primary target of fluoroquinolone antimicrobial agents is the A subunit of DNA gyrase. In several cases a close relationship to ID50 (inhibitory dose-50%) and minimum inhibitory concentration (MIC) has been shown for gram-negative bacteria, although this has not been regularly observed for gram-positive bacteria to date. Cellular entry is by means of diffusion and involves, at least in part, the **porin** pathway in the outer membrane of gram-negative bacteria. An energy dependent efflux occurs which is more active in brain heart infusion broth than nutrient broth and which, to date, has not been shown to contribute to inhibition of growth or bacterial lethality. The extent of uptake by different gram-negative bacteria varies and may contribute in some cases to determination of the MIC. Resistance to fluoroquinolones is by means of mutations affecting the gyrase gene coding for the A subunit and mutations which affect cell permeability particularly involving **porin** proteins of the outer membrane. Combined target and permeability resistance has been reported but involves two or more mutational steps. Resistance during clinical treatment has been observed, but is most likely to be of low magnitude and to be detected in patients with significantly compromised host defenses. (28 Refs.)

Tags: Human

Descriptors: Anti-Infective Agents--pharmacology--PD; * **Gram-Negative Bacteria** --metabolism--ME; 4-Quinolones; Anti-Infective Agents --pharmacokinetics--PK; Bacterial Outer Membrane Proteins--metabolism--ME; Cell Membrane Permeability--drug effects--DE; DNA Topoisomerases, Type II --genetics--GE; DNA Topoisomerases, Type II--metabolism--ME; Drug Resistance, Microbial--genetics--GE; Mutation

CAS Registry No.: 0 (4-Quinolones); 0 (Anti-Infective Agents); 0 (Bacterial Outer Membrane Proteins)

Enzyme No.: EC 5.99.1.3 (DNA Topoisomerases, Type II)

Record Date Created: 19890414

Record Date Completed: 19890414

7/9/24 (Item 24 from file: 155)
DIALOG(R) File 155:MEDLINE(R)
(c) format only 2004 The Dialog Corp. All rts. reserv.

08012275 PMID: 2536626

Crystallization and preliminary X-ray analysis of porin from Rhodobacter capsulatus.

Nestel U; Wacker T; Woitzik D; Weckesser J; Kreutz W; Welte W
Institut fur Biophysik und Strahlenbiologie der Albert-Ludwigs-Universita t, Freiburg i.Br., FRG.

FEBS letters (NETHERLANDS) Jan 2 1989, 242 (2) p405-8, ISSN 0014-5793 Journal Code: 0155157

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed
Subfile: INDEX MEDICUS

Porin monomers of the phototrophic bacterium *Rhodobacter capsulatus* were purified. Crystals were obtained from a solution of **porin** solubilized with the detergent octyltetraoxyethylene within 5 days using the vapor phase equilibration technique. The crystals were rhombohedral with an edge length of 0.4 mm. The space group was trigonal R3 with unit cell constants of $a = b = 95 \text{ \AA}$, $c = 147 \text{ \AA}$. Reflexions were observed to 3.2 \AA .

Tags: Support, Non-U.S. Gov't
Descriptors: *Bacterial Outer Membrane Proteins--ultrastructure--UL; Crystallography; **Gram-Negative Bacteria** --analysis--AN; Molecular Weight; **Porins** ; Protein Conformation; X-Ray Diffraction
CAS Registry No.: 0 (Bacterial Outer Membrane Proteins); 0 (Porins)
Record Date Created: 19890316
Record Date Completed: 19890316

7/9/25 (Item 25 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

(c) format only 2004 The Dialog Corp. All rts. reserv.

07998635 PMID: 2850910

Antibiotic uptake into gram-negative bacteria.

Hancock R E; Bell A

Department of Microbiology, University of British Columbia, Vancouver, Canada.

European journal of clinical microbiology & infectious diseases - official publication of the European Society of Clinical Microbiology (GERMANY, WEST) Dec 1988, 7 (6) p713-20, ISSN 0934-9723

Journal Code: 8804297

Document type: Journal Article; Review; Review, Tutorial

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Antibiotics taken up into gram-negative bacteria face two major diffusion barriers, the outer and cytoplasmic membranes. Of these, the former has been most studied and is discussed in detail here. Evidence from antibiotic MIC studies on **porin** -deficient mutants compared with their **porin** -sufficient parent strains has provided strong support for the proposal that some antibiotics, particularly beta-lactams, pass across the outer membrane through the water-filled channels of a class of proteins called **porins** . Nevertheless substantial evidence has accumulated for the importance of non- **porin** pathways of antibiotic uptake across the outer membranes of gram-negative bacteria. Examples discussed include the uptake of polycationic antibiotics via the self-promoted pathway, the uptake of hydrophobic antibiotics in some bacterial species and in mutants of others via the hydrophobic pathway, and the possible importance of poorly understood non- **porin** pathways of uptake of a variety of antibiotics. Other potential barriers to diffusion, including the cytoplasmic membrane, are briefly discussed. (32 Refs.)

Tags: Support, Non-U.S. Gov't

Descriptors: Anti-Bacterial Agents--pharmacokinetics--PK; * **Gram-Negative Bacteria** --metabolism--ME; Bacterial Outer Membrane Proteins--metabolism--ME; Bacterial Outer Membrane Proteins--physiology--PH; Cell Membrane --metabolism--ME; **Porins**

CAS Registry No.: 0 (Anti-Bacterial Agents); 0 (Bacterial Outer Membrane Proteins); 0 (Porins)

Record Date Created: 19890306

Record Date Completed: 19890306

7/9/26 (Item 26 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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07984476 PMID: 3062001

Bacterial resistance to antibiotics as a function of outer membrane

permeability.

Nikaido H
Department of Microbiology and Immunology, University of California,
Berkeley 94720.

Journal of antimicrobial chemotherapy (ENGLAND) Jul 1988, 22 Suppl A
p17-22, ISSN 0305-7453 Journal Code: 7513617

Document type: Journal Article; Review; Review, Tutorial

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The outer membrane of Gram-negative bacteria serves as barrier to permeation. Transport across this barrier often occurs through channels created by **porins**. Changes in these **porins** can account for antibiotic resistance. The combination of a permeability barrier and beta-lactamases in the periplasmic space leads to a situation in which concentrations, at the target, of even third-generation cephalosporins, can be significantly decreased. (35 Refs.)

Descriptors: Cell Membrane--physiology--PH; *Cell Membrane Permeability;
*Drug Resistance, Microbial; * **Gram-Negative Bacteria** --physiology--PH;
Anti-Bacterial Agents--pharmacology--PD; **Gram-Negative Bacteria** --drug
effects--DE; **Gram-Negative Bacteria** --genetics--GE

CAS Registry No.: 0 (Anti-Bacterial Agents)

Record Date Created: 19890223

Record Date Completed: 19890223

7/9/27 (Item 27 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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07967307 PMID: 2849372

Structure and function of porins from gram-negative bacteria.

Benz R

Lehrstuhl für Biotechnologie der Universität Würzburg, Federal Republic
of Germany.

Annual review of microbiology (UNITED STATES) 1988, 42 p359-93,
ISSN 0066-4227 Journal Code: 0372370

Document type: Journal Article; Review; Review, Academic

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

(142 Refs.)

Tags: Support, Non-U.S. Gov't

Descriptors: Bacterial Outer Membrane Proteins--analysis--AN; *
Gram-Negative Bacteria --ultrastructure--UL; Amino Acid Sequence;
Bacterial Outer Membrane Proteins--ultrastructure--UL; Cell Membrane
--analysis--AN; Cell Membrane--ultrastructure--UL; **Gram-Negative Bacteria**
--analysis--AN; Molecular Sequence Data; **Porins**

CAS Registry No.: 0 (Bacterial Outer Membrane Proteins); 0 (Porins)

Record Date Created: 19890117

Record Date Completed: 19890117

7/9/28 (Item 28 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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07935317 PMID: 2460910

Structure and functions of the cell envelope of gram-negative bacteria.

Nikaido H

Department of Microbiology and Immunology, University of California,
Berkeley 94720.

Reviews of infectious diseases (UNITED STATES) Jul-Aug 1988, 10 Suppl
2 pS279-81, ISSN 0162-0886 Journal Code: 7905878

Contract/Grant No.: AI 09644; AI; NIAID

Document type: Journal Article; Review; Review, Tutorial

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The surface of gram-negative bacteria contains structures that prevent the entry of noxious compounds into the cell and that help the cell evade recognition by host elements such as antibodies and complement while allowing the bacteria to obtain nutrients from the environment and to attach to structures of the host cell. This review discusses the role of outer-membrane components such as lipopolysaccharides and **porin**, as well as appendages such as capsules and fimbriae in such functions. (13 Refs.)

Tags: Human; Support, U.S. Gov't, P.H.S.

Descriptors: **Gram-Negative Bacteria** --ultrastructure--UL; Animals; Bacterial Outer Membrane Proteins--metabolism--ME; Cell Membrane --physiology--PH; Cell Membrane--ultrastructure--UL; **Gram-Negative Bacteria** --physiology--PH; Ion Channels; Polysaccharides, Bacterial --physiology--PH; **Porins**

CAS Registry No.: 0 (Bacterial Outer Membrane Proteins); 0 (Ion Channels); 0 (Polysaccharides, Bacterial); 0 (Porins)

Record Date Created: 19881212

Record Date Completed: 19881212

7/9/29 (Item 29 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

(c) format only 2004 The Dialog Corp. All rts. reserv.

07935267 PMID: 3142011

Permeation of beta-lactam antibiotics into Escherichia coli, Pseudomonas aeruginosa, and other gram-negative bacteria.

Livermore D M

Department of Medical Microbiology, London Hospital Medical College, United Kingdom.

Reviews of infectious diseases (UNITED STATES) Jul-Aug 1988, 10 (4) p691-8, ISSN 0162-0886 Journal Code: 7905878

Document type: Journal Article; Review; Review Literature

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Cell wall impermeability is a major determinant of the susceptibility of gram-negative bacilli to beta-lactam antibiotics. The outer membrane, which beta-lactam agents cross via pores composed of **porin** proteins, is the major individual barrier in the wall structure but does not of itself exclude these antibiotics. Rather, it slows their influx to a level that the periplasmic clearance mechanisms may manage to contain. The clearance mechanisms include hydrolysis and perhaps covalent binding by beta-lactamases and nonessential penicillin-binding proteins. The balance between uptake and clearance determines the fate of the cell, rather than one or the other factor alone. It is possible to represent this interplay mathematically for *Escherichia coli*, but *Pseudomonas aeruginosa* presents a more ambivalent picture. Moreover, the relations among **porin** quantity, permeability, and resistance are much better established for *E. coli* than for *P. aeruginosa*, and the possible existence of additional barrier layers--besides the outer membrane--in the latter species cannot be excluded. (59 Refs.)

Tags: Support, Non-U.S. Gov't

Descriptors: Anti-Bacterial Agents--pharmacology--PD; *Cell Membrane Permeability; **Escherichia coli*--drug effects--DE; * **Gram-Negative Bacteria** --drug effects--DE; **Pseudomonas aeruginosa*--drug effects--DE; Anti-Bacterial Agents--metabolism--ME; Cell Membrane--drug effects--DE; Cell Membrane--metabolism--ME; *Escherichia coli*--metabolism--ME; *Escherichia coli*--ultrastructure--UL; **Gram-Negative Bacteria** --metabolism--ME; **Gram-Negative Bacteria** --ultrastructure--UL; Lactams; *Pseudomonas aeruginosa*--metabolism--ME; *Pseudomonas aeruginosa*--ultrastructure--UL

CAS Registry No.: 0 (Anti-Bacterial Agents); 0 (Lactams)

Record Date Created: 19881213

Record Date Completed: 19881213

7/9/30 (Item 30 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

(c) format only 2004 The Dialog Corp. All rts. reserv.

07881026 PMID: 2901351

Permeation of hydrophilic molecules through the outer membrane of gram-negative bacteria. Review on bacterial porins .

Benz R; Bauer K

Lehrstuhl fur Biotechnologie, Universitat Wurzburg, Federal Republic of Germany.

European journal of biochemistry / FEBS (GERMANY, WEST) Sep 1 1988,

176 (1) p1-19, ISSN 0014-2956 Journal Code: 0107600

Document type: Journal Article; Review; Review, Academic

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

(259 Refs.)

Tags: Support, Non-U.S. Gov't

Descriptors: Bacterial Outer Membrane Proteins--metabolism--ME; *Cell Membrane Permeability; * **Gram-Negative Bacteria** --metabolism--ME; Bacterial Outer Membrane Proteins--biosynthesis--BI; Bacterial Outer Membrane Proteins--classification--CL; Bacterial Outer Membrane Proteins--isolation and purification--IP; Diffusion; Lipid Bilayers--metabolism--ME; Liposomes --metabolism--ME; Membrane Potentials; **Porins** ; PrPSc Proteins; Viral Proteins--isolation and purification--IP

CAS Registry No.: 0 (Bacterial Outer Membrane Proteins); 0 (Lipid Bilayers); 0 (Liposomes); 0 (Porins); 0 (PrPSc Proteins); 0 (Viral Proteins)

Record Date Created: 19881021

Record Date Completed: 19881021

7/9/31 (Item 31 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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07835707 PMID: 3260854

Emergence of resistance during beta-lactam therapy of gram-negative infections. Bacterial mechanisms and medical responses.

Pechere J C

Departement de Microbiologie, Centre Medical Universitaire, Geneve.

Drugs (UNITED STATES) 1988, 35 Suppl 2 p22-8, ISSN 0012-6667

Journal Code: 7600076

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Some Gram-negative, non-fastidious bacilli, although classified as susceptible by conventional susceptibility testing methods, become resistant during therapy with the newer beta-lactam compounds. Emergence of resistance results primarily from the selection of resistant clones pre-existing within the susceptible bacterial populations. Most of the resistant clones produce large amounts of beta-lactamases which inhibit the beta-lactam antibiotics by hydrolysis, rather than by binding. In addition, resistant clones can limit the penetration of beta-lactam molecules through the outer membrane by a decreased expression of their **porins** . Less commonly, when beta-lactamase activity together with alteration of the permeability barrier does not prevent the access of the antibiotic molecules to their target, altered penicillin-binding proteins (PBPs) can produce resistance. However, the risk of resistance emerging during therapy varies with the beta-lactam drug administered. Some compounds such as cefpirome, BMY 28142, SCH 34343, or imipenem appear to be associated with a low risk. In addition, emergence of resistance can be reduced by using higher dosages of beta-lactam agents, or by combining them with other drugs such as aminoglycosides or quinolones.

Tags: Support, Non-U.S. Gov't

Descriptors: *Anti-Bacterial Agents--therapeutic use--TU; *Bacterial

Proteins; *Drug Resistance, Microbial; *Hexosyltransferases;
*Peptidyltransferase; *Peritonitis--drug therapy--DT; Animals; Carrier
Proteins--metabolism--ME; Cell Membrane Permeability; Disease Models,
Animal; Enzyme Induction; **Gram-Negative Bacteria** --metabolism--ME; Lactams
; Mice; Mice, Inbred ICR; Muramoylpentapeptide Carboxypeptidase--metabolism
--ME; Penicillins--metabolism--ME; beta-Lactamases--biosynthesis--BI
CAS Registry No.: 0 (Anti-Bacterial Agents); 0 (Bacterial Proteins);
0 (Carrier Proteins); 0 (Lactams); 0 (Penicillins)
Enzyme No.: EC 2.3.2.12 (Peptidyltransferase); EC 2.4.1.-
(Hexosyltransferases); EC 3.4.16.4 (penicillin-binding protein); EC
3.4.17.8 (Muramoylpentapeptide Carboxypeptidase); EC 3.5.2.6
(beta-Lactamases)
Record Date Created: 19880907
Record Date Completed: 19880907

7/9/32 (Item 32 from file: 155)
DIALOG(R) File 155:MEDLINE(R)
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07600814 PMID: 2445170

**The porin protein of the outer membrane of Escherichia coli: reactivity
in immunoblotting, antibody-binding by the native protein, and
cross-reactivity with other enteric bacteria.**

Henriksen A Z; Maeland J A
Department of Microbiology, Faculty of Medicine, University of Trondheim,
Norway.

Acta pathologica, microbiologica, et immunologica Scandinavica. Section
B, Microbiology (DENMARK) Oct 1987, 95 (5) p315-21, ISSN 0108-0180
Journal Code: 8206623

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The experimental conditions for antibody-binding by the 38.5 kD **porin**
protein of an E. coli 055 strain in immunoblotting were investigated. A
non-ionic detergent in the buffer which contained the primary antibody was
required for antibody-binding by electroblots of the SDS-denatured protein.
Immunoblotting, using antiserum absorbed with bacteria or the outer
membrane (OM) of the E. coli 055 strain, showed results concordant with
inaccessibility to antibodies of the 38.5 kD **porin** protein in its native
configuration in the bacterial cells, but immunoreactivity when contained
in the OM. OM from strains of different genera of the Enterobacteriaceae
and antisera against these strains when used in immunoblot analyses showed
that the E. coli 055 **porin** protein harboured antigenic determinants which
are common to the various genera of the enteric bacilli. Cross-reactivity
with non-enteric Gram-negative bacteria was not observed.

Descriptors: *Antibodies, Bacterial--immunology--IM; *Antigens, Bacterial
--immunology--IM; *Bacterial Outer Membrane Proteins--immunology--IM;
*Enterobacteriaceae--immunology--IM; *Escherichia coli--immunology--IM;
Cross Reactions; Epitopes; **Gram-Negative Bacteria** --immunology--IM;
Immunoassay; **Porins**

CAS Registry No.: 0 (Antibodies, Bacterial); 0 (Antigens, Bacterial);
0 (Bacterial Outer Membrane Proteins); 0 (Epitopes); 0 (Porins)

Record Date Created: 19871130

Record Date Completed: 19871130

7/9/33 (Item 33 from file: 155)
DIALOG(R) File 155:MEDLINE(R)
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07422674 PMID: 3032781

**Antibody-independent killing of gram-negative bacteria via the classical
pathway of complement.**

Loos M; Clas F

Immunology letters (NETHERLANDS) Feb 1987, 14 (3) p203-8, ISSN
0165-2478 Journal Code: 7910006

Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS

The experiments in this paper provided evidence that, besides lipopolysaccharides (LPS), **porins** of gram-negative bacteria bind to C1q and C1. From these experiments, we concluded that the association of LPS and **porins** (outer membrane proteins, OMP) may potentiate the C1q and C1 binding in the absence of specific antibodies. This antibody independent binding of C1 to LPS and **porins** is a prerequisite for the activation of the classical pathway of complement leading to the killing of serum-sensitive bacteria.

Descriptors: Bacteriolysis; *Complement 1--metabolism--ME; ***Gram-Negative Bacteria** --immunology--IM; Bacterial Outer Membrane Proteins --metabolism--ME; Complement 1q; Complement Activating Enzymes--metabolism --ME; Lipopolysaccharides--metabolism--ME; **Porins** ; Protein Binding
CAS Registry No.: 0 (Bacterial Outer Membrane Proteins); 0 (Complement 1); 0 (Lipopolysaccharides); 0 (Porins); 80295-33-6 (Complement 1q)
Enzyme No.: EC 3.- (Complement Activating Enzymes)
Record Date Created: 19870602
Record Date Completed: 19870602

7/9/34 (Item 34 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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07367800 PMID: 2434461

Role of porins in outer membrane permeability.

Hancock R E

Journal of bacteriology (UNITED STATES) Mar 1987, 169 (3) p929-33,

ISSN 0021-9193 Journal Code: 2985120R

Document type: Journal Article; Review

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

(49 Refs.)

Tags: Support, Non-U.S. Gov't

Descriptors: Bacterial Outer Membrane Proteins--metabolism--ME; *Cell Membrane Permeability; * **Gram-Negative Bacteria** --metabolism--ME; *Ion Channels--metabolism--ME; Models, Molecular; **Porins** ; Protein Conformation

CAS Registry No.: 0 (Bacterial Outer Membrane Proteins); 0 (Ion Channels); 0 (Porins)

Record Date Created: 19870406

Record Date Completed: 19870406

7/9/35 (Item 35 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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07155810 PMID: 3013502

Outer-membrane permeability of bacteria.

Nakae T

Critical reviews in microbiology (UNITED STATES) 1986, 13 (1) p1-62,

ISSN 1040-841X Journal Code: 8914274

Document type: Journal Article; Review

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Gram-negative bacteria evolved to survive under the conditions in which a number of hazardous compounds are abundant. The outer membrane which protects the cell interior acts as a barrier against such hazardous agents, yet the cells must incorporate the chemicals that are essential for the cellular activity. The devices that Gram-negative bacteria developed to incorporate such essence are the transmembrane pores. These pores could be

subdivided into three categories: (1) pore made of **porins** has a weak solute selectivity; (2) pore made of lamB protein and tsx proteins hold intermediate solute specificity. and (3) pores for the diffusion of vitamin B12 and ferric ion-chelator complexes have a tight solute specificity.

Porins are identified from a number of Gram-negatives and from the outer membrane of mitochondria of various sources. Studies on the diffusion properties of these outer-membrane proteins provided essential information to understand membrane transports. (302 Refs.)

Tags: Support, Non-U.S. Gov't

Descriptors: Bacterial Outer Membrane Proteins--metabolism--ME; *Cell Membrane Permeability; * **Gram-Negative Bacteria** --metabolism--ME; Anti-Bacterial Agents--metabolism--ME; Bacterial Outer Membrane Proteins--analysis--AN; Bacterial Outer Membrane Proteins--biosynthesis--BI; Bacterial Outer Membrane Proteins--genetics--GE; Cell Membrane--analysis--AN; Cell Membrane--metabolism--ME; Cell Membrane--ultrastructure--UL; Chloroplasts--metabolism--ME; Chloroplasts--ultrastructure--UL; Enterobacteriaceae--drug effects--DE; Enterobacteriaceae--genetics--GE; Enterobacteriaceae--metabolism--ME; Enterobacteriaceae--ultrastructure--UL; Ferric Compounds--metabolism--ME; Gene Expression Regulation; Genes, Bacterial; **Gram-Negative Bacteria** --drug effects--DE; **Gram-Negative Bacteria** --genetics--GE; **Gram-Negative Bacteria** --ultrastructure--UL; Lipids --metabolism--ME; Lipopolysaccharides--analysis--AN; Mitochondria--analysis--AN; Mitochondria--metabolism--ME; Mutation; Phosphates--metabolism--ME; Phospholipids--analysis--AN; **Porins** ; Pseudomonas aeruginosa--metabolism--ME; Pseudomonas aeruginosa--ultrastructure--UL; Receptors, Virus --metabolism--ME; Temperature; Vitamin B 12--metabolism--ME

CAS Registry No.: 0 (Anti-Bacterial Agents); 0 (Bacterial Outer Membrane Proteins); 0 (Ferric Compounds); 0 (Lipids); 0 (Lipopolysaccharides); 0 (Phosphates); 0 (Phospholipids); 0 (Porins); 0 (Receptors, Virus); 0 (lambda phage receptor); 0 (protein K); 68-19-9 (Vitamin B 12)

Record Date Created: 19860811

Record Date Completed: 19860811

7/9/36 (Item 36 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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06966184 PMID: 2415299

Porin from bacterial and mitochondrial outer membranes.

Benz R

CRC critical reviews in biochemistry (UNITED STATES) 1985, 19 (2) p145-90, ISSN 0045-6411 Journal Code: 0330403

Document type: Journal Article; Review

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The outer membrane of gram-negative bacteria acts as a molecular filter with defined exclusion limit for hydrophilic substances. The exclusion limit is dependent on the type of bacteria and has for enteric bacteria like *Escherichia coli* and *Salmonella typhimurium* a value between 600 and 800 Daltons, whereas molecules with molecular weights up to 6000 can penetrate the outer membrane of *Pseudomonas aeruginosa*. The molecular sieving properties result from the presence of a class of major proteins called **porins** which form trimers of identical subunits in the outer membrane. The **porin** trimers most likely contain only one large but well-defined pore with a diameter between 1.2 and 2 nm. Mitochondria are presumably descendents of gram-negative bacteria. The outer membrane of mitochondria contains in agreement with this hypothesis large pores which are permeable for hydrophilic substances with molecular weights up to 6000. The mitochondrial **porins** are processed by the cell and have molecular weights around 30,000 Daltons. There exists some evidence that the pore is controlled by electric fields and metabolic processes. (296 Refs.)

Tags: Support, Non-U.S. Gov't

Descriptors: *Bacterial Outer Membrane Proteins; *Mitochondria --metabolism--ME; Amino Acid Sequence; Animals; Bacterial Outer Membrane Proteins--isolation and purification--IP; Bacterial Outer Membrane

Proteins--metabolism--ME; Cell Membrane--metabolism--ME; Cell Membrane
--ultrastructure--UL; Cell Membrane Permeability; Chloroplasts--metabolism
--ME; Escherichia coli--metabolism--ME; **Gram-Negative Bacteria**
--metabolism--ME; Intracellular Membranes--metabolism--ME; Ion Channels
--metabolism--ME; Lipid Bilayers; Macromolecular Systems; **Porins**
CAS Registry No.: 0 (Bacterial Outer Membrane Proteins); 0 (Ion
Channels); 0 (Lipid Bilayers); 0 (Macromolecular Systems); 0 (Porins)
Record Date Created: 19860123
Record Date Completed: 19860123

7/9/37 (Item 37 from file: 155)
DIALOG(R) File 155:MEDLINE(R)
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06950539 PMID: 2414604
Role of ionic events in the triggering of phagocytosis.
Young J D
Journal of theoretical biology (ENGLAND) Oct 7 1985, 116 (3) p475-8,
ISSN 0022-5193 Journal Code: 0376342
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
Tags: Support, Non-U.S. Gov't
Descriptors: *Phagocytosis; Bacterial Outer Membrane Proteins; Calcium;
Endocytosis; **Gram-Negative Bacteria**; Ion Channels; **Porins**; Receptors,
Fc
CAS Registry No.: 0 (Bacterial Outer Membrane Proteins); 0 (Ion
Channels); 0 (Porins); 0 (Receptors, Fc); 7440-70-2 (Calcium)
Record Date Created: 19851216
Record Date Completed: 19851216

7/9/38 (Item 38 from file: 155)
DIALOG(R) File 155:MEDLINE(R)
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06833836 PMID: 2408719
**Characterization of two surface-localized antigenic sites on porin
protein F of Pseudomonas aeruginosa.**
Mutharia L M; Hancock R E
Canadian journal of microbiology (CANADA) Apr 1985, 31 (4) p381-6,
ISSN 0008-4166 Journal Code: 0372707
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
A rapid colony immunoblot screening procedure was used to demonstrate the
surface localization of **porin** protein F on bacterial colonies of
Pseudomonas aeruginosa. By this method, we demonstrated that protein F was
accessible to four different specific monoclonal antibodies in a wide
variety of both mucoid and nonmucoid P. aeruginosa strains. Controls were
performed to demonstrate that, using this procedure, only surface-exposed
epitopes bound monoclonal antibodies and that nonspecific binding of
monoclonal antibodies either to cells lacking protein F or to mucoid
exopolysaccharide did not occur. Monoclonal antibodies MA4-4, MA2-10, and
MA4-10, specific for protein F, also interacted with colonies of
Pseudomonas putida and Pseudomonas syringae, whereas the protein F specific
monoclonal antibody MA5-8 interacted only with P. aeruginosa strains. Using
the above-named monoclonal antibodies, we investigated the antigenic
structure of protein F. Monoclonal antibodies MA4-4, MA2-10, and MA4-10
bound to 29-31 kilodalton proteolytic fragments produced after papain or
trypsin digestion of purified protein F or of protein F in outer membranes
or intact cells. Antibody MA5-8 did not interact with proteolytically
digested protein F but did interact with two of the six fragments produced
after partial cyanogen bromide cleavage of protein F. Antibodies MA4-4,

MA2-10, and MA4-10 did not interact with protein F after reduction of its internal disulphide bonds with 2-mercaptoethanol; in contrast, the reactivity of MA5-8 was unaffected. This data suggests that there are at least two distinct highly conserved surface epitopes on **porin** protein F.

Tags: Support, Non-U.S. Gov't

Descriptors: *Antigens, Surface--immunology--IM; *Bacterial Outer Membrane Proteins--immunology--IM; *Epitopes--analysis--AN; *Pseudomonas aeruginosa--immunology--IM; Antibodies, Monoclonal; Antigens, Bacterial --immunology--IM; Cross Reactions; **Gram-Negative Bacteria** --immunology--IM; Peptide Hydrolases--pharmacology--PD; **Porins** ; Pseudomonas--immunology --IM; Species Specificity

CAS Registry No.: 0 (Antibodies, Monoclonal); 0 (Antigens, Bacterial); 0 (Antigens, Surface); 0 (Bacterial Outer Membrane Proteins); 0 (Epitopes); 0 (Porins)

Enzyme No.: EC 3.4 (Peptide Hydrolases)

Record Date Created: 19850812

Record Date Completed: 19850812

7/9/39 (Item 39 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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06743354 PMID: 6098767

Permeability properties of the outer membrane of gram-negative bacteria--a discover of porin .

Nakae T.

Kitasato archives of experimental medicine (JAPAN) Apr 1984, 57 (1)
p1-20, ISSN 0023-1924 Journal Code: 0376613

Document type: Journal Article; Review

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

(35 Refs.)

Tags: Support, Non-U.S. Gov't

Descriptors: Bacterial Outer Membrane Proteins--physiology--PH; ***Gram-Negative Bacteria** --ultrastructure--UL; Cell Membrane--analysis--AN; Electrophoresis, Polyacrylamide Gel; Escherichia coli--ultrastructure--UL; Lipid Bilayers; Membrane Proteins--analysis--AN; Models, Biological; Models, Molecular; Molecular Weight; Mutation; Permeability; Phospholipids; **Porins** ; Salmonella--ultrastructure--UL

CAS Registry No.: 0 (Bacterial Outer Membrane Proteins); 0 (Lipid Bilayers); 0 (Membrane Proteins); 0 (Phospholipids); 0 (Porins)

Record Date Created: 19850405

Record Date Completed: 19850405

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 \$0.02 Estimated cost File467
 OneSearch, 26 files, 0.708 DialUnits FileOS
 \$0.24 TELNET
 \$10.89 Estimated cost this search
 \$10.89 Estimated total session cost 0.708 DialUnits

Status: Signed Off. (1 minutes)